

**FIG. 1**

[illegible]





FIG. 1 Continued

TGCCCCGGCTGGAGCTCCTGTCCAGGAACGGACACATGTGGCTGCCAGTGCAGCCACACAGCCAGCTTTGCGGTGC  
TCATGGATAATCTCCAGGCGTGAGAACGGGAGGCTCCTGCTCTGAAGATTGTCACTATGCCCTGTGTCTTGTCACTG  
GCAGCCCTGCTGTGGCTTTCCTCTCTGAGCTGCTGCGCATGCTGCGCTCCAACCTGCACAGCATTACACAGCACCT  
CGCCGTGGCGCTCTTCTCTCAGCTGGTGTTCGTGATTGGGATCAACAGAGCGAAACCGCTTCTGTGCACAGTGG  
TTGCCATCCTCTCCACTACATCTACATGAGCACCTTTGCCCTGGAACCTGCTGGAGAGCCCTGCATGTCTACCGCATGCTG  
ACCGAGGTGCCCAACATCGAACACGGGGCCCATGGGCTTCTACTACGTCTGTGGCTGGCGCATCCCGCCATTGTACAGG  
ACTGGCGGTGGGCTGGACCCCAAGGCTACGGGAACCCGACTTCTGCTGGCTGTGGCTTCAAGACACCTGTATTTGA  
GCTTTGGGGGCCCATCGAGCTGTATATATCATCAACACAGTCACCTTCTGTCTATCTGCAAGGTTTCTGCCAAGA  
AAGCACCATATATATGGGAAAAAGGGATCTCTCCTGCTGAGGACCCCATCTCTCTGCTGTCTCATCAAGCCAC  
CTGGCTGCTGGGCTGCTGGCTGTGAACCGCTATGCACTGAGCTTTCACTACCTCTTCCGCATCTTCAGCCGCTTACAGG  
GGCCCTTCTCTCTCTTTCCTACTGCTGTCAACAGGAGGTCCGGAGCACCTGAAGGGGCTGCTGGCGGGGAGGAAG  
CTGCACCTGGAGGACTCCGCCACCAACAGGCGCACCTCTGAGCGGCTCCCTCACTGCAACACACCTTCCGTGACGG  
GCTGTACATCTGCTGCACAGACTTGGGGGAGTCCACCGCTCTGCTGGACAGCATCTGTAGGGATGAAGGGATCCAGAGC  
TCGGCTGTCTCTGGGCTGGTGGGGGAGCCACGAGAGGCCAGACGGTCCCTCATGCCCAAGGCTGCAAGGATCCC  
CCTGGCCACATTCCTCACTACATAGCGAGCTGTCTCTGATGAGCAGAGCAGCTCTTACGGCTCTCACACTCTGTCA  
CAGCCAGGACCATGGGTGGGAGCTGAGGAAAAATGGGACCCGCGCAGGGGCGCCGTCCACAGCACCCCAAGGGGAGC  
CTGTGGCCACCACTTCCGGCCGGCTGGGCCGAGCAGAGCTGGCTGACAGTCACTGTAGGACCCAGCGGCAAGGCC  
CGCTGAGGATGGAGACCAAGGTGAGCTGTGAGCTGCAACCGGAGGAGCAGGGCAGTCACCGTGGAGAGTACCCCCGGA  
CCAGGAGAGCGGGGCCAGCCAGCTTCTAGCAGCCAGCCCCAGAGCAGAGGAAGGCATCTTCAAAAATTAAGTCA  
CTACCCCTCCCGCTGACGCTGACGGAGCAGCGCTGAAGGGCCGGCTCCGGGAGAACTGGCCGACTGTGAGCAGAGC  
CCACATCTCGGCGACGTCTTCTCTGGGCTGTGGCGCCCGGACTGCCCATCACAGTCAGAGGCTTGGAGGGAGGC  
GGGCTGTACCACTCAACGGGTGGCCATGAATGTCTGCTGAGAGCCCGAGCCGATGCTCCGACTCTGAGAAAC  
CGTGA

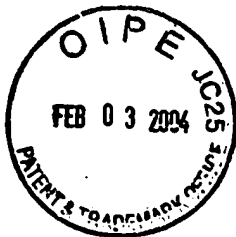


FIG. 2

M A P P P P V L V I L L L L A A A A L P A M C L R A A A W E P R V P G O T R A P A L R P C C T Y A V G A A C T P R A P K E L L O V G F D G R L A G R R K V S  
C A C R P L P L Q V R L V A R S A P T A L S R R L R A R T H L P C G A R A R L C G T G A R L C G A L C P P V P G C A A Q H E A L A A P T T L P A C R C P P  
R P A P C P G R P I C L P P G O S V R L R L L C A L R A A G A V A V G L A E A T A G T P S A S P S P P P L P P H L P E A R A G P A R R A R R G T S G R  
G S L F P M P S Y Q V A L F E H E P A G T L I L Q L H A Y T I E G E E R V S Y M E G L F D E R E R G T F R I D S A T G A V S I D S V L D R E T K E T H V  
L K V K A V D Y S T P P R A S T T Y I T V L V K D T M D S P V F E Q S Y R E R V R E L E V G Y E V L T R A S O R D S P I N A N L E Y R V L G G A M D V F  
Q L N E S P C V V S T R A V L D R E A A E Y Q L L V E A N D O G R P C P L S A T A V Y I E V E D E N D A Y P P S E Q N Y V V Q V P E D U G L N T A V L B  
V O A T D R O G G O N A I H Y S I L S G N V A C Q P Y L H S L S G I L D V I N P L D P E D V Q K Y S L S I K A O G G R P P L I N S G C V S V Q V L D V R D  
M E P I P V S S P P Q A T V L E N V P L C Y P V V H I Q A V D A D S G E N A R L H Y L V D T A S T F L G G S A G P K N E A P T P D P P P Q I H S S G M T  
V C A B L O R E V E N T S P Q V K A V D E G S P P M S S T S V S I T V L V N D E D S V F T Q P T Y E L R L E D A A V G S S V L T Q A R D R A N S V I  
T T Q L T G C N T R R F A L S S Q R G G C L I T L A L P L D Y E Q Q V L A V T A S D G T R S H T A H V L I N V I D A N T H R F V P Q S S H Y T V S V E R  
D R F V G T S I A T L S A M E D T G E N A R I T Y I Q D P V P Q R I D P S O T M Y T M E L D Y E N Q V A T T L T D A Q D B Q I P Q R S D T T T L B I  
L I L D A N D A P Q L N D F T Q G S I P E D A P P S T S I L Q V S A T D R D S C P N O R L Y T P Q G G D G D G D F T I E P T S G V I R T O R L D R E N  
V A V Y N L A L A V D R O S P T L S A S V E I Q V T L O I N D A P H P E K D E L L V E E N P V G S V V A K I R A N D P D E G P H A Q I N Y Q I V E  
G E M R H P Q L D L A B C D L R A N V E L D P E V R E Y V L V Q A T S A P L V S R A T V H I L L V D Q N D P P V L E D P Q I L P M N Y V T N K S N S P P  
T O V I O C I P A H D P D V S D S L N Y T P P Q G N E L R L L L L D P A T G E L Q L S R D L D N P O L E A L M E V S V S D Q I H S V T A P C T L A V T I T D  
D M L T N S I T V L E R N S Q E K F L S P L L A L F V E G V A A V L S T T D O V P V F V H Q N D I V S B N I L N V T P S A L L P G O V R Q P P F S E D L  
Q E Q I Y L N E T L A T T I S T O R V L P T D N I C L R E F C E N Y M E C V S L R P D S S A P L S S P T V L F R P I N P I N G L R C R C P P G P T Q D V C  
E T E I D L C Y S D P G A N U R C A S R E G G Y T C E C P E D T G E H C E V D A R S O R C A N G V C K N G O T C V N L I G G P H C V C P P G E Y E R P Y C  
E V T P R E P P Q S P V T P R E L R O R F H P T I S I A T A T Q E R N G L L Y N G R F N E K H D F I A L E I V D E Q V L T P S A G E T T T T V A P K V S  
G V S D G R M H E V Q V Y T N K P N I G H L G L F H O P S G E R M A V V T D C D T T M A V R F G K D I G N Y S C A A Q Q T Q T G S K S L D L T G P I L L  
Q O V N L P E D F P V H N R Q F V G C M R L S V D G K N V D A G F I A N N G T R E G C A K R R F C D G R C O N G O T C V N E N G M Y L C A C P L R F G  
G K N C E Q A N P H P Q L F S G E S V V S W S D L N I I S V P W I L Q L M P R T R K E D S V L M E A T S C G P T S F R L Q I L N Y L O F E V S H G P S D V S  
S V M L S Q L R V T D G E M H I L L T E L K N V K E D S E M H L V T I L D Y C M D O N K A D I G G M L P O L T V R S V V G G A S E D K V S V R R G P R C C  
M Q C V R N G C T P T N V A T L N D N A L K V R V K D G C D V D P C T S S P C P M S R C H D A M E D Y S C V C D R G Y L G I N C V D A C H L P C E R N O  
A C V R S P G S P Q G Y V C E C G P S H Y G F Y C E N K L O L P C P R A M M O N P V C G P C B C A V S K O F D P D C N K T S O C C K E N Y Y K L L A Q D T C  
L E C D C P P H G S H S R T C D A T G C C A C K P G V I G R Q C N R C D N P F A E V T T L O C E V T Y N G C P K A F E A C I N N P Q T K P G Q P A A V P C P K  
Q S V G N A V R U C S C E K G M L P P E L F N C T T I S F V O L R A M E K L S N E T Q V D C A R A L O L V R A L S A T O N T G T L P G N D V R T A Y Q L L  
G H V L Q H S W Q Q G Y D L A A T O D A D P H E D V I H S G S A L L A P A T R A A M E Q I Q R S E G G T A Q L L E R L E G Y T S V A R N V R T Y L R P P V  
I V T A M I L A V D I P D K F N P T G A R V P R F O T I H E Z P P R E L S S V S P A D F P R P P E K E G P L L R P A G E R T T P O T T R P G P G T E R E  
A P L S R R R R R P D D A G Q F A V A L V I I T R T L O Q L L F E R Y D P D R S L R L P H R P I I N T P M V S T L V S E C A P L R P L R P V L V R F A L  
L E V B E R T K P V C V F M N H S L A V G G T G G W S A R G C E L L S R N R T H V A C Q C S H T A S F A V L M D I S R R E G E V L F L K I V T T A A V S L S L  
A A L L V A P V L L S L V R M L A S N L H S I H K H L A V A L P L S Q L V P I G I N Y T E N P F L C T V V A I L L H Y I Y N S T T A W L V E S L H V Y R L

S E V R N I D T G M R F Y V V G M P I A I V T Q L A V G L D P Q C Y G N P D F C M L S L Q D T L I N S F A G F I G A V I I I N T V T S V L S A K V S C R  
K H H Y G K G I V S L R T A F I L L L I E A I N L L G L L A V N R D A L S P H Y L F A I P S G L Q G P F V L L P H C V L N Q E V R X H L A G V L G R K  
I H L E D S A T T R A T L L T R S L N C N T P P G O G P M L R T M L G B S T A S L O S I V R D E G T O K L G V S E G L V R G S H G E P D A B L M P R S C O P  
P O H D S D S D S L S L D E Q S S Y A S S H S S D E D G V G A E E N D P A R G A V H S T P E G D A V A N H V P A G H P D O S L A E S D S E D P S G K P  
R L K V E T K V S V E L H R E Q G S H R G E Y P P D Q E G G A R L A S S Q P P B O R K O I L K H V T Y P P L T L T E Q T L K G R L R E K L A D C E Q S  
P T S E R T S S I G S G G P D C A I T V E S P C R E P C R H L A N G V A N V E T O S A Q A D G S D E K P



FIG. 3

Score = 939 (140.9 bits), Expect =  $4.0e-81$ , Sum P(3) =  $4.0e-81$   
Identities = 203/218 (93%), Positives = 203/218 (93%), Strand = Plus / Plus

Query: 230 CTGTAAATAGACCAACGCGCAGTCCCAAT-GCAGCGAGATTACTACAAGCTCCTAGCCC 288  
CTG A T A A C GGC TG C T OCA GGAGATTACTACAAGCTCCTAGCCC  
Sbjct: 38281 CTGAAGTCACAGGCGCTGCTCTGCTTTTGA-GGAGATTACTACAAGCTCCTAGCCC 38339

Query: 289 AGGACACCTGTCTGCCCTGCGACTGCTTCCCCCATGGCTCCACAGCCGCACTTGGGACA 348  
AGGACACCTGTCTGCCCTGCGACTGCTTCCCCCATGGCTCCACAGCCGCACTTGGGACA  
Sbjct: 38340 AGGACACCTGTCTGCCCTGCGACTGCTTCCCCCATGGCTCCACAGCCGCACTTGGGACA 38399

Query: 349 TGCCACCGGGCAGTGTGCTGCAAGCCCGCGTCATCGGCGGCCAGTGCACCCGCTGCG 408  
TGCCACCGGGCAGTGTGCTGCAAGCCCGCGTCATCGGCGGCCAGTGCACCCGCTGCG  
Sbjct: 38400 TGCCACCGGGCAGTGTGCTGCAAGCCCGCGTCATCGGCGGCCAGTGCACCCGCTGCG 38459

Query: 409 ACAACCCGTTTGCCGAGGTACCAAGCTCGGCTGTGAAG 467  
ACAACCCGTTTGCCGAGGTACCAAGCTCGGCTGTGAAG  
Sbjct: 38460 ACAACCCGTTTGCCGAGGTACCAAGCTCGGCTGTGAAG 38498



FIG. 4

Score = 1000 (352.0 bits), Expect = 2.4e-98, P = 2.4e-98  
Identities = 162/186 (87%), Positives = 172/186 (92%), Frame = +3

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Query:      3 YLGINCVDAChLNPCENMGACVRSFGSPQGYVCBOGFSHYOPYCENKLDLPCFPGWNGNP 182
              Y G  CVDAC LNPC+++ ACVRSP +P+GY CBCCP HYG YCENK+DLPCP+GWNGNP
Sbjct: 1917 YPGKCKVDACLLNPKKHVAACVRSPNFFRGYSCBOGFGHYGYCENKVDLPCPKGWAGNP 1976

Query:     183 VCGPCHCAVSQGFDPDCNKTNGQCCKENYYKLLAQDTCLPCDCFPHGSHSRTCNATGQ 362
              VCGPCHCAVS+GFDPDCNKTNGQCCKENYYK AQD CLPCDCFPHGSHSR CDM TCG
Sbjct: 1977 VCGPCHCAVSQGFDPDCNKTNGQCCKENYYKPPAQDACLPDCFPHGSHSRACDMDTGQ 2036

Query:      61 CCTGGGTGCGCTCCCCCGGCTCCCCGCAGGGCTACGTGTGCGAGTGTGCCCCCAGTCACT 120
              |||||
Sbjct: 33445 CCTGGGTGCGCTCCCCCGGCTCCCCGCAGGGCTACGTGTGCGAGTGTGGGCCAGTCACT 33504

Query:     121 ACGGCCCGTACTGTGAGAACAA 142
              |||||
Sbjct: 33505 ACGGCCCGTACTGTGAGAACAA 33526
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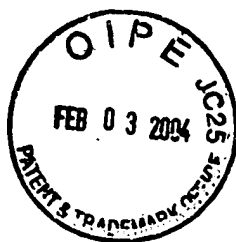


FIG. 5

Score = 12924 (4549.5 bits), Expect = 0.0, P = 0.0  
Identities = 2451/3034 (80%), Positives = 2677/3034 (88%)

Query: 1 MAPPPFPVLPVLLLLAAAAALPAGLRAAAWSPRVPGGTRAFALPFGCTYAVGAACTPR- 59  
MAP P VLP L+LLAAAA LPA+ L AAANE RVPGG RAFAL PG +Y + TPR  
Sbjct: 1 MAPSSPRVLPALVLLAAAA-LPALELGAAWELRVPGGARAPALPGWNYRLDTTPTRE 59  
Query: 60 ---APRELLOVGRD-GRLAGRRRVSG-AGRPLFLOVRLVARSAPTALSRLRARTHLPGC 114  
RE GR G AG + AGR LPLQVRLVAR APTA S LRAR + C  
Sbjct: 60 LLOVSREGPAAGRRLGLGAGTLOCARLAGRLPLQVRLVARGAPTAPSLVLRARAYGARC 119  
Query: 115 GARA-RICGTGRL-----CG-ALCFPVPGGCAAAQHSALAAPTLPACRCPPRP 162  
G R R GA.L G ALCFP OG AA+ S L A T PAC CPP  
Sbjct: 120 GVLLLRBARGAELRSPAVRSVPGLGDALCFPAAGGGAASITVLEAITNTPACSCPPVA 179  
Query: 163 RPRCPGRPICLPFGSSVRLRLCALRRAAGAVRVGLALEAATAGTPSASPSPSPLPPLNL 222  
C PICL PGCS LRL-CAL RAAGAV V L ++A T+GTPS SPS SP L NL  
Sbjct: 180 GTCRRROPICLRPGGSARLRLVLCALGRAAGAVVVELVIA- TSGTPSSEPSVSPSLL-NL 237  
Query: 223 PEARAGPARRAROTSGRQSLKFPFMYQVALFENEPAQTLLQLHAHTTIEGSEERVS 282  
+ KAG RR+RRT 8 +FP+P+YQV++ KNEPAGT +++L AH BG+ R+SY  
Sbjct: 238 SQPRAGVVRRSRRTGSGSTSPQFPLPSYQVSENEPAGTAVIELRAHDFDEGDAGRLSY 297  
Query: 283 YMBGLFDRSRGYFRIDSATGAVSTDVLDRETKETHVLKVKAVDYSTPPRSATTYITVL 342  
ME LFDERS GYP ID+ATGAV+T LDRETK+THVL+V AVD+ +P RSA TY+TV  
Sbjct: 298 QMBALFDRSRGYFLIDAATGAVTTARSLDRETKDTHVLKVS AVD+GSPRSATTYITVT 357  
Query: 343 VKDTNHSFVPEQSEYREVRNLEVGVEVLTIRASDRDSPINANLRYRVLOGANDVFL 402  
V DTNHSFVPEQSEYREK+RNLVGVYEVLTIRA+D D+P MAN+RYR+L GA VF++  
Sbjct: 358 VSDTNHSFVPEQSEYREVRNLEVGVEVLTIRATDGDAPENARMRYRLLEGAGGVFEI 417  
Query: 403 NBSGCVVSTRAVLDRKEAAYQLLVEANDQGRNPGPLSATATVYIVEDENDNYPQFSEQ 462  
+ SGVV TRAV+DRKEAAYQLLVEANDQGRNPGPLSA+ATV+I VEDENDNYPQFSE+  
Sbjct: 418 DARGGVVTRAVVDRKEAAYQLLVEANDQGRNPGPLSASATVHIVVEDENDNYPQFSEK 477  
Query: 463 NYVQVQFEDVGLNTAVLKVQATDRDQGNAAIHYSILSGNVAGQFYLHSLSGILDVINPL 522  
YVQVQFEDV +NTAVLKVQATDRDQGNAAIHYSI+SGH+ GQFYLHSLSG LDVINPL  
Sbjct: 478 RYVQVQFEDVAVNTAVLKVQATDRDQGNAAIHYSIVSGHLKQFYLHSLSGSLDVINPL 537  
Query: 523 DFEVQKYSLSIKAQDQGRPFLINSQVSVQVLDVNDNEPIFVSSPFOATVLENVFLGY 582  
DFE +++Y+L IKAQDQGRPFLINSQ+SVQVLDVNDN PIFVSSPFOA VLENVFLG+  
Sbjct: 538 DFEALREYTLRIKAQDQGRPFLINSQGLVSVQVLDVNDNAPIFVSSPFOAVLENVFLGH 597  
Query: 583 PVVHIQAVDADSGENARLHYRLVDTASTYLCGGSAGPKNPAPTDFPFQIHNSSGNITVC 642  
V+HIQAVDAD+GENARL YRLVDTAST +GG S +NPA DPFQIHNSSGNITVC  
Sbjct: 598 SVLHIQAVDADAGENARLQYRLVDTASTIVGCSVDSENPAAPDFPFQIHNSSGNITVC 657  
Query: 643 AELDREVEHYSPGVEAVDHGSPMSSTSVSITVLDVNDNDPVFTQPTYELRLNEDAAV 702  
AELDREVEHYSPGVEAVDHGSP MS88 SVSITVLDVNDNDP+FTQF YELRLNEDAAV  
Sbjct: 658 AELDREVEHYSPGVEAVDHGSPMS88SVSITVLDVNDNDPFTQFVYELRLNEDAAV 717  
Query: 703 GSSVLTLQARDRANSVITYQLTGNTKRFALSSQSGGLITLALFLDYKQBQYVLA 762  
GSSVLTL+AKDRANSVITYQLTGNTKRFALSSQ CGGLITLALFLDYKQB+QYVLA  
Sbjct: 718 GSSVLTLRARDRANSVITYQLTGNTKRFALSSQSGGLITLALFLDYKQBQYVLA 777  
Query: 763 TASDGTSHHTAHVLIINVTDANTHRPVQSSHYTVSVSEDRPVGTSIATLSANEDTGENA 822  
TASDGTSHHTA V INVTDANTHRPVQSSHYTVSVSEDRPVGTSIAT+SA DEDTGENA  
Sbjct: 778 TASDGTSHHTAQVFINVTDANTHRPVQSSHYTVSVSEDRPVGTSIATISATDGTGENA 837  
Query: 823 RITYVTQDPVPQFRIDPDSQMTYTHMELDYEMQVAYTLITMAQNGIPQKSDTTLLEILI 882  
RITYV++DPVPQFRIDP+GT+YTH ELDYE+Q AYTL I AQNGIPQKSDT+LEILI  
Sbjct: 838 RITYVLEDPVPQFRIDPDTGTITHTMELDYEDQAAYTLITMAQNGIPQKSDTTLLEILI 897



## FIG. 5 Continued

Query: 883 LDANDNAPQFLNDFYQGSIFEDAPPSTSILOVSATDRDSCGPNRLLYTFQGGDDGDDFY 942  
LDANDNAP+FL DFPQGS+PEDAPPSTS+LQVSATDRDSCGPNRLLYTFQGGDDGDDFY  
Sbjct: 898 LDANDNAPFLRDFYQGSVPEDAPPSTSVLQVSATDRDSCGPNRLLYTFQGGDDGDDFY 957

Query: 943 IEPTSGVIRTQRLDRENVAVYNLWALAVDRGSPPLSASVEIQVTILDINDNAPMFKD 1002  
IEPTSGVIRTQRLDRENVAVYNLWALAVDRGSP PLSASV IQV++LDINDN P+YKCD  
Sbjct: 958 IEPTSGVIRTQRLDRENVAVYNLWALAVDRGSPNPLSASVGIQVSVLDINDNPFVFKD 1017

Query: 1003 ELLEFVEENFVGVSVVAKIRANDPDEGPNQAQIYQIVEGDMRHFQOLDLNGDLRAMVEL 1062  
ELLEFVEEN+FVGVSVVA+IRANDPDEGPNQAQI+YQIVEG++ FQLDLL+GDLRA+VEL  
Sbjct: 1018 ELLEFVEENFVGVSVVAKIRANDPDEGPNQAQIYQIVEGDMRHFQOLDLNGDLRAMVEL 1077

Query: 1063 DFEVRREYVLVVOATSAFLVSRATVHILLVDQNDNPFVLPDFQILFNNYVTNKSNSFPTG 1122  
DFEVR+Y+LVVOATSAFLVSRATVHI L+QNDNPF LPDFQILFNNYVTNKSNSF+G  
Sbjct: 1078 DFEVRDYMLVVOATSAFLVSRATVHILLVDQNDNPFVLPDFQILFNNYVTNKSNSFPG 1137

Query: 1123 VIGCIPANDPDVSDSLNYTFVQGNELRLLLLDPATGELQLSRDLDRNPLEALNEVSVD 1182  
VIG IPANDPD+SDSLNYTF+QGNEL LLLLDPATGELQLSRDLDRNPLEALNEVSVD  
Sbjct: 1138 VIGRIPANDPDVSDSLNYTFVQGNELRLLLLDPATGELQLSRDLDRNPLEALNEVSVD 1197

Query: 1183 GIHSVTAFCTLRVTIITDMLTNSITVLEENMSQKFLSPILLALFVBGAANVLSTTKDDV 1242  
GIHSVTA CTLRVTIITDMLTNSITVLEENMSQKFLSPILL+LFVBGA VLESTTKDD+  
Sbjct: 1198 GIHSVTALCTLRVTIITDMLTNSITVLEENMSQKFLSPILLSLFVBGAATVLESTTKDDI 1257

Query: 1243 FVFNVQNDTDVSSNMLSVTFSSALLPGGVROQFPFSEDLOEQIYLNRTLLTTISTORVLPF 1302  
FVFNV+QNDTDVSSNMLSVTFSSALLPGG RQ+FPFSEDLOEQIYLNRTLLTTIS QRVLPF  
Sbjct: 1258 FVFNIQNDTDVSSNMLSVTFSSALLPGGTRGRFPFSEDLOEQIYLNRTLLTTISQRVLPF 1317

Query: 1303 DNNICLREPCENYMKCVSVLRFDSSAPFLSSTTVLFRPIHPINGLRCRCPPGFTGDCYET 1362  
DNNICLREPCENYMKCVSVLRFDSSAPF+SSTTVLFRPIHPI GLRCRCPPGFTGDCYET  
Sbjct: 1318 DNNICLREPCENYMKCVSVLRFDSSAPFLSSTTVLFRPIHPITGLRCRCPPGFTGDCYET 1377

Query: 1363 EIDLCEYEDPCGANGRCRSEGGYTCBCFEDFTGHECEVDARSGBRCANGVCKNGGTCVNL 1422  
EIDLCEY+PCGANGRCRSEGGYTCBCFEDFTGHEC+V+ RSCRC+GVCKNGGTCVNL  
Sbjct: 1378 EIDLCEYSPGANGRCRSEGGYTCBCFEDFTGHECQVNVRSGBRCASGVCKNGGTCVNL 1437

Query: 1423 IGGPHCVCPFGSEYRPHYCEVSTRSFPFQSFVTFRGLRQRFHPTISLFPATQERNGLLLYN 1482  
IGGPHCVCPFGSEYRPHYCEV+TRSFPPQSFVTFRGLRQRFHPT+SL FATQ+RN LLLYN  
Sbjct: 1438 IGGPHCVCPFGSEYRPHYCEVSTRSFPFQSFVTFRGLRQRFHPTVELAFATQERNGLLLYN 1497

Query: 1483 GRFNEKHDFIALRIV+BQ+QLTFSAGETTTTVAFKVPFGVSDGRNHSVQVQYNEKNIGH 1542  
GRFNEKHDFIALRIV+BQ+QLTFSAGETTTTVA P+VF CVDGRNHSV VQYNEKNIGH  
Sbjct: 1498 GRFNEKHDFIALRIVEBQLQLTFSAGETTTTTPQVFGVSDGRNHSVQVQYNEKNIGH 1557

Query: 1543 LGLPHGPGSEKMAVVTVDCCDTMAVRFGKDIGNYSCAAQGTQTSKKSLLDTGPIILGG 1602  
LGLPHGPGSEK+AVVTVDCCD +AV FG +GNYSCAAQGTQ+GSKKSLLDTGPIILGG  
Sbjct: 1558 LGLPHGPGSEKMAVVTVDCCDAAVAVHFGSYVCNYSCAAQGTQSGSKKSLLDTGPIILGG 1617

Query: 1603 VFNLPEDFPVHNRQFVOCNRLSVDCNVDMAAFIANGTRECCEARRNFCDDRCCNGG 1662  
VFNLPEDFPVH+RQFVOCNRLS+DG+ VDMA FIANGTRECCEARRNFCDDRCCNGG  
Sbjct: 1618 VFNLPEDFPVHNRQFVOCNRLSIDGRIVDMAAFIANGTRECCEARRNFCDDRCCNGG 1677

Query: 1663 TCVNRNMYLCECPLRFGGKCEQAMPHQPLFSGESVVSNDLNIISVFNILGLMFRTR 1722  
TCVNRNMYLCECPLRFGGKCEQAMPHQ P+GESVVSNDL+I ISVFNILGLMFRTR  
Sbjct: 1678 TCVNRNMYLCECPLRFGGKCEQAMPHQPLFSGESVVSNDLNIISVFNILGLMFRTR 1737





## FIG. 5 Continued

Query: 2563 VRNIDTGMRFYFVVGNGIPAIUTGLAVGLDPQGTGNPDPFCWLSLQDTLINSFAGPICAV 2622  
VRNIDTGMRFYFVVGNGIPAIUTGLAVGLDPQGTGNPDPFCWLSLQDTLINSFAGP+G V  
Sbjct: 2578 VRNIDTGMRFYFVVGNGIPAIUTGLAVGLDPQGTGNPDPFCWLSLQDTLINSFAGPVQTV 2637

Query: 2623 IIINTVTSVLSAKVSCQRKHYYGKKGIVSLRTAFLLLLLISATWLLGLLAVNRDALSF 2682  
IIINTV VLSAKVSCQRKHYY +KG+VE+LRTAFLLLLL++ATWLLGLLAVN D LSF  
Sbjct: 2638 IIINTVIFVLSAKVSCQRKHYYERKGVVSMRTAFLLLLLVATWLLGLLAVNSDTLSF 2697

Query: 2683 HYLFAIPSCLOGPFFVLLPHCVLNQEVKHLKGVLCGRKLHLEDSATTRATLLTRSLNCF 2742  
HYLFA FS LQC FVLLPHCV ++EVRKHL+ VL C+KL L+DSATTRATLLTRSLNCF  
Sbjct: 2698 HYLFAAFSCLOGIFVLLPHCVAHREVRKHLRAVLGKKLQDDSATTRATLLTRSLNCF 2757

Query: 2743 TFGDCPMLRTDLGESTASLDSIVRDEGIQKLGVSGLVRGSHQEPDASLMFRSCKDPPG 2802  
T+ +GPDMLRT LGESTASLDS RDEG+QKL VSSG RG+HGEFD S +PR+ K C  
Sbjct: 2758 TYSEGPDMLRTALGESTASLDSITRDEGVQKLVESGPARCNHGEFDTSFIPRSEKKAHG 2817

Query: 2803 HDSDSSELSLDEQSSSYASSHSSDSEDDGVGAREKNDPARGAVHSTFKGDAVANHVPAQ 2862  
DESDSELSLDE 66SYASSH+SDSEDDG AE+KM+PA G HSTPK DA+ANHVPAQ  
Sbjct: 2818 PDSDELSLDEHSSSYASSHTSDSEDDGGAEDKMPAGGPAHSTFKADALANHVPAQ 2877

Query: 2863 WPDQSLAESDSEDPGKPKLVETKVSVELHREKQSHRGEYFPDQESGGAAR---LASS 2919  
WPD+SLA SDSE+ +P LKVETKVSVELHR+ QG+H G+ P D ESG A+ + SS  
Sbjct: 2878 WPDSELAGSDSEKELDTEPHLKVETKVSVELHRQAQGNHCGDRPSOPESGVLAKEPVAVLS 2937

Query: 2920 QPPEQRKGLKDKVITYPPFLTLTBTQTLKGLREKLADCEQSPTSSRTSSLCSC---GPD 2975  
QP EQKQILKDKVITYPPFL EQ LK RLREKLADCEQSPTSSRTSSLCSC D  
Sbjct: 2938 QPQEQKGLKDKVITYPPFLP--EQPLKSLREKLADCEQSPTSSRTSSLCSGDQVHATD 2995

Query: 2976 CAITVKEPGRGPHLNGVAMNVRTGSAQADGSDSEKP 3014  
C-IT+K+P-REPGR+HLNGVAMNVRTGSAQA+GSDSEKP  
Sbjct: 2996 CVITIKTPRREPGRHNGVAMNVRTGSAQANGSDSEKP 3034



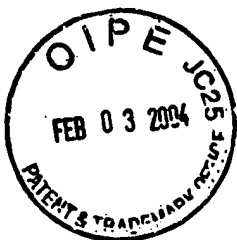


FIG. 8

MEFVRALWLGALALGPGSAGGHPOFCGYLARLGGSVRLGALLPRAPLARARARAALARAALAPRLPH  
NLSELEVVAAPPARDPASLTRGLQALVPPGVAALLAFPEARPELLQLEHFLAAATETPVLSELRREBARAP  
LGAPNPFHLQLEHWASPLETLDDVLYAVLQAHAWEDVGLALCKTQDPGLVALWTSRAGEPPQLVLDLS  
RRDTGDAGLEARLAPMAAFVGGEAPVPAAVLLGCDIARARRVLEAVPPGPHWLLGTPLFPKALPTAGLP  
POLLALGEVARPPLAAIHDIQVVARALQSAAQVQPKRALLPAPVNCDDLQAGFESPGRFLARFLANT  
SPQGRTPGVVWVTQSSPDEDGQCPAGQLCLDPGTNDSATLDALPAALANGSAPRALRKCCYGYCIDLER  
LAEDTFFDFELYLVGDOKYGALRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTSPFTSTSLGI  
MVRARDTASPIGAFMWPLHWSTWLOVFAALHLTALFLTVYEWSPYGLTPRGNRSTVFSYSSALNLC  
YAILFRRTVSSEKTPKCPTRILLMNLWAFCLLVLSSTANLAAMVGDKTPEELSGHDPKGRFOTVWE  
SEABAYDKSFPMHAHMRHSAPTTPROVAMLTSDPPKLNAPMDKSLLDYEVSIDADCKLLTVGKPF  
AIBGYGGLPQNSPLTSNLSEFISRYESSGFIDLHDKWYEMVPCGKRVPAVTEILOMSTYHFAGLFVLLC  
LGLGSALLSSLGEHAFFRLALPRIRKOSRLQYWLHTSQKIHREALNTEPPEOSKEETAAEAEPSCHEVEQQQ  
QDQPTAPEGWKRARRAVDKERRYRFLLEPAVVVAPEADAEAAAPREGFVWLCYGRPPAARFTGAP  
QFGELEERIEVARHRLQALVERGOQLAQLODSARHRFRLLQARAAPAEAPHSGRPGSQE

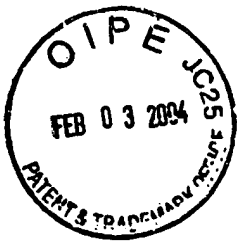


FIG. 9

Score = 3832 (575.0 bits), Expect = 0.0, Sum P(S) = 0.0  
Identities = 928/1076 (86%), Positives = 928/1076 (86%), Strand = Plus / Plus

Query: 788 CACTGCCGCCCCAAGCCCTGCCACCGCGGGCTGCCACCAGGCTGCTGGCGCTGGGCG 847  
C CTGCC CC A G CCTG CCA C CG CT CCA GC C GGC C G G G  
Sbjct: 22736 CCGTCCC-CCTAGGTTCTGCGCCACACGTC-CTTCCAGGCGCGCA-CGGGCCCCGGTGTG 22792

Query: 848 AGGTGGCAGC-ACCCCGCTGC-AGGCC-G-C-CATC-CATGACATTGTGCAACTGGTGC 901  
GGTG CA G A C CC C G G A C G C C C C T A TGTG A C T G  
Sbjct: 22793 -GGTGACAGGCAGCTCC-CAGGTACACATGTCTCGGCACTTTAAGGTGTGGAGCT-TCG 22849

Query: 902 CCGGGGCGCT-GGGCAGTGGCGGCCAGGTGCAGCGGAGCGAGCCCTCTCCCGGCCCCG 960  
CC GG C C GGG G C G CC GG CA C G G AGC C C GCG G  
Sbjct: 22850 CCGGACCCACGGGCGGCTCCGGGCTGGGCCA-CGGTGGGCACTGGCGGGACGGCCA-G 22907

Query: 961 GTCAACTGCCGGGACCTGCAGCCGCGCGCGCGCGAGTCCCCGGGGCG-CTTCTTGGCAG 1019  
T ACT GG ACC G AG G C GC CG G CCCC C C TG C G  
Sbjct: 22908 CTGGACTT--GGACCGGGAGGTGCTCTGCACG-GCCCCGCCCCACAGGGGTGGCCAG 22964

Query: 1020 GTTCTGCGCC-AA-CA-CGTCTTCCAGGCCGACACGGC-CCCCGTGGGTGACAGCA 1075  
GT CTGGCC AA C CGT T A GC G G C CCC T TG GT G C  
Sbjct: 22965 GT-CTGGCCCAAGCTGCGTG-TGGTAACGCTGTTGGAAACACCCATTGTGTTT-GCCC 23019

Query: 1076 GCTCCCGAGAGCAAGACGGGCAUTGCCACCGGGGCACTGTGCTGGACCCCTGGCACCA 1135  
G CCGAGCGAAGACGGGCACTGCCACGGGGCACTGTGCTGGACCCCTGGCACCA  
Sbjct: 23020 GTGATCCAGAGCAAGACGGGCAUTGCCACCGGGGCACTGTGCTGGACCCCTGGCACCA 23079

Query: 1136 AGCACTCGGCCACCCCTGGACCGCACTGTTCGCGCGCTGGCCAAAGGCTCAGCCCCCGTG 1195  
AGCACTCGGCCACCCCTGGACCGCACTGTTCGCGCGCTGGCCAAAGGCTCAGCCCCCGTG  
Sbjct: 23080 AGCACTCGGCCACCCCTGGACCGCACTGTTCGCGCGCTGGCCAAAGGCTCAGCCCCCGTG 23139

Query: 1196 CCTGCGCAAGTGTCTACGGCTACTGCACTGACCTGCTGGAGCGGCTGGCGGAGGACA 1255  
CCTGCGCAAGTGTCTACGGCTACTGCACTGACCTGCTGGAGCGGCTGGCGGAGGACA  
Sbjct: 23140 CCTGCGCAAGTGTCTACGGCTACTGCACTGACCTGCTGGAGCGGCTGGCGGAGGACA 23199

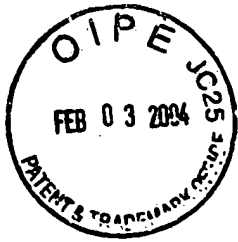
Query: 1256 CGCCCTTGGACTTGGAGCTGTACCTCGTGGGTGACGGCAAGTACGGGCGGCTGGCGGAGC 1315  
CGCCCTTGGACTTGGAGCTGTACCTCGTGGGTGACGGCAAGTACGGGCGGCTGGCGGAGC  
Sbjct: 23200 CGCCCTTGGACTTGGAGCTGTACCTCGTGGGTGACGGCAAGTACGGGCGGCTGGCGGAGC 23259

Query: 1316 CCGCTGCAACCGGCTGGTCCGGCACTGCTGCCCGGCGGCGCCACATGGCGGTACCA 1375  
GCGCTGCAACCGGCTGGTCCGGCACTGCTGCCCGGCGGCGCCACATGGCGGTACCA  
Sbjct: 23260 GCGCTGCAACCGGCTGGTCCGGCACTGCTGCCCGGCGGCGCCACATGGCGGTACCA 23319

Query: 1376 GCTTCAGTATCAACTCGCGCGCTCAGAGGTGGTGGACTTCACAGCCCTTCTTCTCCA 1435  
GCTTCAGTATCAACTCGCGCGCTCAGAGGTGGTGGACTTCACAGCCCTTCTTCTCCA  
Sbjct: 23320 GCTTCAGTATCAACTCGCGCGCTCAGAGGTGGTGGACTTCACAGCCCTTCTTCTCCA 23379

Query: 1436 CCACCCCTCGGCATCATGGTGGCGGCACGGGACACGGGCTCAGCCATCGGTGCTTTATGT 1495  
CCAGCTTGGGCATCATGGTGGCGGCACGGGACACGGGCTCAGCCATCGGTGCTTTATGT  
Sbjct: 23380 CCAGCTTGGGCATCATGGTGGCGGCACGGGACACGGGCTCAGCCATCGGTGCTTTATGT 23439

Query: 1496 GCGCCCTGCACTGGTCCAGGTGGCTGGGCGTCTTTCGCGGCTGCACTCAGCGGCTCT 1555  
GCGCCCTGCACTGGTCCAGGTGGCTGGGCGTCTTTCGCGGCTGCACTCAGCGGCTCT



## FIG. 9 Continued

Sbjct: 23440 GGGCCCTGCACTGGTCCACGTGGCTGGGCGTCTTTGGGGCCCTGCACCTCAACGGCGCTCT 23499

Query: 1556 TCCTCACCGGTGTACGAGTGGCGTAGCCCCCTACGGCCCTCACGGCACGTGGCCGCAACCCCA 1615  
TCCTCACCGGTGTACGAGTGGCGTAGCCCCCTACGGCCCTCACGGCACGTGGCCGCAACCCCA

Sbjct: 23500 TCCTCACCGGTGTACGAGTGGCGTAGCCCCCTACGGCCCTCACGGCACGTGGCCGCAACCCCA 23559

Query: 1616 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGGCATCCTCTTCAGACGCA 1675  
GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGGCATCCTCTTCAGACGCA

Sbjct: 23560 GCACCGTCTTCTCCTACTCCTCAGCCCTCAACCTGTGCTACGGCATCCTCTTCAGACGCA 23619

Query: 1676 CCGTGTCCAGCAAGACGCCCAAGTGGCCACGGCCCGCTGCTCATGAACCTCTGGGCCA 1735  
CCGTGTCCAGCAAGACGCCCAAGTGGCCACGGCCCGCTGCTCATGAACCTCTGGGCCA

Sbjct: 23620 CCGTGTCCAGCAAGACGCCCAAGTGGCCACGGCCCGCTGCTCATGAACCTCTGGGCCA 23679

Query: 1736 TCTTCTGCTGCTGGTGTCTGTCCAGCTACACGGCCCAACCTGGCTGCGGTTCATGGTGGGG 1795  
TCTTCTGCTGCTGGTGTCTGTCCAGCTACACGGCCCAACCTGGCTGCGGTTCATGGTGGGG

Sbjct: 23680 TCTTCTGCTGCTGGTGTCTGTCCAGCTACACGGCCCAACCTGGCTGCGGTTCATGGTGGGG 23739

Query: 1796 ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCAAGGGCTTCGGCTTCGGCACCG 1855  
ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCAAGG C GC TGG

Sbjct: 23740 ACAAGACCTTCGAGGAGCTGTGCGGGATCCACGACCCCAAGGTGGGCGGCTTCGGCGGC 23799

Query: 1856 TGTGGAG 1863  
TG GGG G

Sbjct: 23800 TGGGGTG 23807



FIG. 10

Score = 2426 (854.0 bits), Expect = 0.0, Sum P(2) = 0.0

Identities = 463/474 (97%), Positives = 464/474 (97%), Frames = +1

Query: 1063 WVTGSSFDGQCPAGQLCLDPGTND SATLDALFAALANGSAPRALRRCCTGYCIDLLER 1242  
+V FDEDGQCPAGQLCLDPGTND SATLDALFAALANGSAPRALRRCCTGYCIDLLER  
Sbjct: 427 FVFANDPDEDGQCPAGQLCLDPGTND SATLDALFAALANGSAPRALRRCCTGYCIDLLER 486

Query: 1243 LAEDTFPDPFELTLVGDKYKALRDGRWTLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 1422  
LAEDTFPDPFELTLVGDKYKALRDGRWTLVGDLLAGRAHMAVTSFSINSARSQVVDFTS  
Sbjct: 487 LAEDTFPDPFELTLVGDKYKALRDGRWTLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 546

Query: 1423 PFFSTSLGINVRARDTASPIGAFMPLHNSIWLGVFAALHLTALFLTVYENRSFYGLTPR 1602  
PFFSTSLGINVRARDTASPIGAFMPLHNSIWLGVFAALHLTALFLTVYENRSFYGLTPR  
Sbjct: 547 PFFSTSLGINVRARDTASPIGAFMPLHNSIWLGVFAALHLTALFLTVYENRSFYGLTPR 606

Query: 1603 GNRSTVFSYSSALNLCYAILPRTVSSKTFKCP TGRLLMNLWAI FCLLVLSSTYANLAA 1782  
GNRSTVFSYSSALNLCYAILPRTVSSKTFKCP TGRLLMNLWAI FCLLVLSSTYANLAA  
Sbjct: 607 GNRSTVFSYSSALNLCYAILPRTVSSKTFKCP TGRLLMNLWAI FCLLVLSSTYANLAA 666

Query: 1783 VMVGDKTFEELSGIHDPK-----CFRPGTVWESSAEAYIKKSFPMHMHMRHSAPTFP 1944  
VMVGDKTFEELSGIHDPK CFRPGTVWESSAEAYIKKSFPMHMHMRHSAPTFP  
Sbjct: 667 VMVGDKTFEELSGIHDPK LHPAQCPRPGTVWESSAEAYIKKSFPMHMHMRHSAPTFP 726

Query: 1945 RGVANLPSDPPKLNAPIMDKSLLDYEVSIDADCKLLTVGKPPAIBGYGIGLPQNSPLTSN 2124  
RGVANLPSDPPKLNAPIMDKSLLDYEVSIDADCKLLTVGKPPAIBGYGIGLPQNSPLTSN  
Sbjct: 727 RGVANLPSDPPKLNAPIMDKSLLDYEVSIDADCKLLTVGKPPAIBGYGIGLPQNSPLTSN 786

Query: 2125 LSEFISRYKSSGFIDLLHDKWYKMPVCGKRVFAVTETLQMSIYHFAGLFVLLCIGLSAL 2304  
LSEFISRYKSSGFIDLLHDKWYKMPVCGKRVFAVTETLQMSIYHFAGLFVLLCIGLSAL  
Sbjct: 787 LSEFISRYKSSGFIDLLHDKWYKMPVCGKRVFAVTETLQMSIYHFAGLFVLLCIGLSAL 846

Query: 2305 LSSLGSHAFFRLALPRIKGSRLQYWLHTSQKIHRAINTEPPEGSKKEETAER 2466  
LSSLGSHAFFRLALPRIKGSRLQYWLHTSQKIHRAINTEPPEGSKKEETAER  
Sbjct: 847 LSSLGSHAFFRLALPRIKGSRLQYWLHTSQKIHRAINTEPPEGSKKEETAER 900









FIG. 13

MEFVRALWGLALALGPGSAGGHPQCOVLARLOGSVRLGALLPRAFLARARARAALARAALAPRLPH  
NLSLELVYAAPPARDPASLTRGLQCALVFPQVAALLAFPEARPELLQLHFLAAATEIPVLSLRREARAP  
LGAPNPHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTQDPGGLVALWTSRAGRPPQLVLDLS  
RRDTGDAGLRARLAPMAAPVGGEAPVPAAVLLOCDIARARRVLEAVPPGPHWLLGTPLPKALPTAGLP  
PGLLALGEVARPFLAAIHDIQVLVARALGSAAQVQPKRALLPAPVNOGDLQAPGESPGRFLARFLANT  
SFQGRTPGVVWTGSSPDEDGGCPAGQLCLDPGTINDSATLDALFAALANGSAPRALRKOCYGYCHILLER  
LAEDTPDFELYLVGDKYGAIRDGRWTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTSPFPSTSLGI  
MVRARDTASPIGAPMWPLHWSTWLGVPAAHLHTALFLTVYEWRSPLYGLTPRGNRSTVFSYSSALNLC  
YAILFRRTVSSKTPKCTGRLLMNLWAFCLLVLSSTANLAAMVVGDKTFEELSGHDPKLEHHPAQGR  
PGTVWESSABAYIKKSPDMHAHMRHSAFTTPRGVAMLTSDPPKLNAFMDKSLLDYEVSIDADCKLL  
TVGKPFABEGYQGLPQNSPLTSNLSEFISRYKSSGFIDLLHDKWYKMPVPCGRVFAVTETLQMSIYHFAO  
LFVLLCLGLSALLSSLGHAFFRLALPRIRKGSRLQYWLHTSQKIRALNTEPPEOSKEETABAEPSGFB  
VEQQQQQDQPTAFEGWKARRAVDKERRYVRLLEPAVVVAPEADAEAAAFREGPVWLCSYGRPPA  
ARPTGAPQGELOELERRIEVARERLRQALVERGQLLAQLGDSARHRPRILLQARAAPAEAPPHSGRPGS  
QB



FIG. 14

Score = 3832 (575.0 bits), Expect = 0.0, Sum P(3) = 0.0  
Identities = 948/1107 (85%), Positives = 948/1107 (85%), Strand = Plus / Plus

Query: 788 CACTGCCGCCCAAGGCCCTGCCCAACGCGGGGCTGCCACCAAGGCTGCTGGCCCTGGGCG 847  
C CTGCC CC A G CCTG CCA C CG CT CCA GC C GGC C G G G  
Sbjct: 22736 CCTGCC-CCTAGGTTCTTCCCAACACGTC-CTCCAGGGCCGCA-CGGGCCCGTGTG 22792

Query: 848 AGGTGGCAGC-ACCCCGCTGG-AGGCC-G-C-CATC-CATGACATTGTGCAACTGGTGG 901  
GGTG CA G A C CC C GG A C G C C C C T A TGTG A C T G  
Sbjct: 22793 -GGTGACAGGCACTCC-CAGGTACACATGTCTCGGCACCTTAAGGTGTGGAGCCT-TG 22849

Query: 902 CCGGGCCCT-GGCAGTGCAGCCCAAGTTCAGCCGAAGCAGCCCTCTCCCGCCCCG 960  
CC GG C C GGG G C G CC GG CA C G G AGC C C GGC G  
Sbjct: 22850 CCGGACCCAGGGGCGCCCCGGCTGGGCCA-CGGTGGGCAGCTGGGGGAGGCCA-G 22907

Query: 961 GTCAACTGCCCGACCTGCAGCCCGCCGGCCGAGTCCCGGGGGG-CTTCTTGGCAGG 1019  
T ACT GG ACC G AG G C GC CG G CCCC C C TG C G  
Sbjct: 22908 CTGGACTT--GGACCGGGAGGTCCCTCTGCACG-GCCCCGCCCCACAGGGTGCOCAG 22964

Query: 1020 GTTCTGGCC-AA-CA-CGTCTTCCAGGGCCGACGGGC-CCCGTGTGGGTGACAGGCA 1075  
GT CTGCC AA C COT T A GC G G C CCC T TG GT G C  
Sbjct: 22963 GT--CTGGCCCAAGCTGCCTG-TGGTAACGCTGTTGGAACCCATTGTGTTT--GCC 23019

Query: 1076 GCTCCCAAGACGAAGACGGGCAGTGCACAGCGGGCAGCTGTGCTTGCACCTGGCACCA 1135  
G CCAGACGAAGACGGGCAGTGCACAGCGGGCAGCTGTGCTTGCACCTGGCACCA  
Sbjct: 23020 GTGATCCAGACGAAGACGGGCAGTGCACAGCGGGCAGCTGTGCTTGCACCTGGCACCA 23079

Query: 1136 ACGACTGGGCCACCTTGGACGCACTGTTGCCCGCGCTGGCCAAAGGCTCAGCGCCCCGTG 1195  
ACGACTGGGCCACCTTGGACGCACTGTTGCCCGCGCTGGCCAAAGGCTCAGCGCCCCGTG  
Sbjct: 23080 ACGACTGGGCCACCTTGGACGCACTGTTGCCCGCGCTGGCCAAAGGCTCAGCGCCCCGTG 23139



## FIG. 14 Continued

Query: 1196 CCCTGCCAAGTGCCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 1255  
CCCTGCCAAGTGCCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA  
Sbjct: 23140 CCCTGCCAAGTGCCTGCTACGGCTACTGCATTGACCTGCTGGAGCGGCTGGCGGAGGACA 23199

Query: 1256 CGCCCTTCGACTTCGAGCTGTACTCTGTTGGGTGACGGCAAGTACGGCGCCCTTCGGGACG 1315  
CGCCCTTCGACTTCGAGCTGTACTCTGTTGGGTGACGGCAAGTACGGCGCCCTTCGGGACG  
Sbjct: 23200 CGCCCTTCGACTTCGAGCTGTACTCTGTTGGGTGACGGCAAGTACGGCGCCCTTCGGGACG 23259

Query: 1315 GCGCTGGAACCGGCTGCTGCGGGACCTGCTGGCGCGCGGCTCCACATGGCGGTACCA 1375  
GCGCTGGAACCGGCTGCTGCGGGACCTGCTGGCGCGCGGCTCCACATGGCGGTACCA  
Sbjct: 23260 GCGCTGGAACCGGCTGCTGCGGGACCTGCTGGCGCGCGGCTCCACATGGCGGTACCA 23319

Query: 1376 GCTTCAGTATCAACTCCGCCGCTCACAGGTGGTGGACTTCACCAAGCCCTTCTTCTCCA 1435  
GCTTCAGTATCAACTCCGCCGCTCACAGGTGGTGGACTTCACCAAGCCCTTCTTCTCCA  
Sbjct: 23320 GCTTCAGTATCAACTCCGCCGCTCACAGGTGGTGGACTTCACCAAGCCCTTCTTCTCCA 23379

Query: 1436 CCAGCTTGGCATCATGGTGCAGGACAGGACACGGCTCACCCATCGGTGCTTTATGT 1495  
CCAGCTTGGCATCATGGTGCAGGACAGGACACGGCTCACCCATCGGTGCTTTATGT  
Sbjct: 23380 CCAGCTTGGCATCATGGTGCAGGACAGGACACGGCTCACCCATCGGTGCTTTATGT 23439

Query: 1496 GGCCCTTCAGCTGGTCCACGTGGCTGGGCTCTTTGGCGCCCTGCACCTCACCGGCTCT 1555  
GGCCCTTCAGCTGGTCCACGTGGCTGGGCTCTTTGGCGCCCTGCACCTCACCGGCTCT  
Sbjct: 23440 GGCCCTTCAGCTGGTCCACGTGGCTGGGCTCTTTGGCGCCCTGCACCTCACCGGCTCT 23499

Query: 1556 TCCTCACCGTGTACGAGTGGCGTAGCCCTACGGCTCACGCCACGTGGCGCAACCGCA 1615  
TCCTCACCGTGTACGAGTGGCGTAGCCCTACGGCTCACGCCACGTGGCGCAACCGCA  
Sbjct: 23500 TCCTCACCGTGTACGAGTGGCGTAGCCCTACGGCTCACGCCACGTGGCGCAACCGCA 23559

Query: 1616 GCACCGTCTTCTCTACTCTCTCAGCCCTCAACCTGTGCTACGCCATCTCTTCAGACGCA 1675  
GCACCGTCTTCTCTACTCTCTCAGCCCTCAACCTGTGCTACGCCATCTCTTCAGACGCA  
Sbjct: 23560 GCACCGTCTTCTCTACTCTCTCAGCCCTCAACCTGTGCTACGCCATCTCTTCAGACGCA 23619

Query: 1676 CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCGGCTGCTCATGAACCTCTGGGCCA 1735  
CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCGGCTGCTCATGAACCTCTGGGCCA  
Sbjct: 23620 CCGTGTCCAGCAAGACGCCCAAGTGCCCCACGGGCGGCTGCTCATGAACCTCTGGGCCA 23679

Query: 1736 TCTTCTGCTGCTGGTGTCTTCCAGCTACACGGCCAACTGGCTGCCGTCTATGGTGGGG 1795  
TCTTCTGCTGCTGGTGTCTTCCAGCTACACGGCCAACTGGCTGCCGTCTATGGTGGGG  
Sbjct: 23680 TCTTCTGCTGCTGGTGTCTTCCAGCTACACGGCCAACTGGCTGCCGTCTATGGTGGGG 23739

Query: 1796 ACAAGACCTTCGAGGAGCTGTTCGGGATCCACGACCCCAAGCTGCACACC-CGGCCAG 1854  
ACAAGACCTTCGAGGAGCTGTTCGGGATCCACGACCCCAAGCTGCACACC-CGGCCAG  
Sbjct: 23740 ACAAGACCTTCGAGGAGCTGTTCGGGATCCACGACCCCAAGCTGCACACC-CGGCCAG 23796

Query: 1855 GGCTTCGGCTTCGGCAACCTGTGGGAGACAGC-CGGAG 1894  
GGCTTCGGCTTCGGCAACCTGTGGGAGACAGC-CGGAG  
Sbjct: 23797 GGCTTCGGCTTCGGCAACCTGTGGGAGACAGC-CGGAG 23834

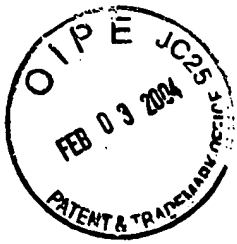


FIG. 15

Score = 2481 (873.4 bits), Expect = 0.0, Sum P(2) = 0.0  
Identities = 469/474 (98%), Positives = 470/474 (99%), Frame = +1

Query: 1063 WVTGSSPEDGQCPCAGQCLDPGTINDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 1242  
+V PDEDQCPCAGQCLDPGTINDSATLDALFAALANGSAPRALRKCCYGYCIDLLER  
Sbjct: 427 FVFARDPDEDGQCPCAGQCLDPGTINDSATLDALFAALANGSAPRALRKCCYGYCIDLLER 486

Query: 1243 LAEDTFFDFELYLVDGQKYGALRDGRNTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 1422  
LAEDTFFDFELYLVDGQKYGALRDGRNTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS  
Sbjct: 487 LAEDTFFDFELYLVDGQKYGALRDGRNTGLVGDLLAGRAHMAVTSFSINSARSQVVDFTS 546

Query: 1423 PFFSTSLGINVRARDTASPIGAPMPLHNSWLGVAALHLTALFLAVYENRSPYGLTPR 1602  
PFFSTSLGINVRARDTASPIGAPMPLHNSWLGVAALHLTALFLAVYENRSPYGLTPR  
Sbjct: 547 PFFSTSLGINVRARDTASPIGAPMPLHNSWLGVAALHLTALFLAVYENRSPYGLTPR 606

Query: 1603 GRNRSTVFSYSSALNLCYAILFRRTVSSKTFECPTGRLMMMAIFCLLVLSSTYANLAA 1782  
GRNRSTVFSYSSALNLCYAILFRRTVSSKTFECPTGRLMMMAIFCLLVLSSTYANLAA  
Sbjct: 607 GRNRSTVFSYSSALNLCYAILFRRTVSSKTFECPTGRLMMMAIFCLLVLSSTYANLAA 666

Query: 1783 VMVGDKTFEELSGIHDPKLHHPAQGFPGTVWESSAEAYIKKSFPDMHAHRRHSAPPTP 1962  
VMVGDKTFEELSGIHDPKLHHPAQGFPGTVWESSAEAYIKKSFPDMHAHRRHSAPPTP  
Sbjct: 667 VMVGDKTFEELSGIHDPKLHHPAQGFPGTVWESSAEAYIKKSFPDMHAHRRHSAPPTP 726

Query: 1963 RGVAMLTSDPPKLNAPINDKSLDYEVSIDADCKLLTVGKPPAIEGTGIGLPQNSPLTSN 2142  
RGVAMLTSDPPKLNAPINDKSLDYEVSIDADCKLLTVGKPPAIEGTGIGLPQNSPLTSN  
Sbjct: 727 RGVAMLTSDPPKLNAPINDKSLDYEVSIDADCKLLTVGKPPAIEGTGIGLPQNSPLTSN 786

Query: 2143 LSEFISRYKSSGFIDLLHDKWYKMFPCGKRVFVAVTETLQNSIYHFAGLFVLLCLGLGSAL 2322  
LSEFISRYKSSGFIDLLHDKWYKMFPCGKRVFVAVTETLQNSIYHFAGLFVLLCLGLGSAL  
Sbjct: 787 LSEFISRYKSSGFIDLLHDKWYKMFPCGKRVFVAVTETLQNSIYHFAGLFVLLCLGLGSAL 846

Query: 2323 LSSLGEHAFPRALPRIRKGSRLQWLHTSQKIHRAHNTPEPESKEETAERAP 2484  
LSSLGEHAFPRALPRIRKGSRLQWLHTSQKIHRAHNTPEPESKEETAERAP  
Sbjct: 847 LSSLGEHAFPRALPRIRKGSRLQWLHTSQKIHRAHNTPEPESKEETAERAP 900







FIG. 18

MEFVRALWLGLALALGPGSAAGGHFQPGVLRARLGGSVRLGAILPRAPLARARARAALARAALAPRLPH  
NLSLELVVAAPPARDPASLTROLCQALVPPGVAALLAPPEARPELLQLHFLAAATETPVLSLLRRRARAP  
LQAPNPFHLQLHWASPLETLLDVLVAVLQAHAWEDVGLALCRTQDPGGLVALWTSRAGRPPQLVLDLS  
RRDTGDAGLRARLAPMAAPVOGEAPVPAAVLLGCDIARARRVLEAVPPGPHWLLGTPLPPKALPTAGLP  
PGLLALGHEVARPPLEAAHEDIVQLVARALGSAAQVQPKRALLPAPVNOGDLQAPGESPGRFLARFLANT  
SFQGRGTGPVWVTGSSQVHMSRHPKVWSLRDRDPRGAPAWATVGSWRDOQLDLEPGGASARPPPPQGAQ  
VWPKLRVVTLLHPPVFARDPDEDGQCPAGQLCLDPTNDSATLDALFAALANGSAPRALRKCCYGYCI  
DLIERLAEDTTPDFELYLVGDGKYGALRDGRWTGLVGDLLAGRAHMAVTSPSINSARSQVVDFTSPFFS  
TSLGIMVRARDTASPIGAPMWPLHWSTWLGVFALHLTALFLTVYEWRSFYGLTPRGNRSTVRSYSSA  
LNLGYALFRRTVSSKTPKCPTGRLLMNLWAIPCLLVLSYTNLAAMVVGDKIFEELSGIHDPKLHHPA  
QGFRPGTVWESSAEBAYIKKSFFDMHAHMRRHSAPTTPRGVAMLTSDPPKLNAFIMDKSLLDYEVSDAD  
CKLLTVGKPPAIBGYGIGLPQNSPLTSNLSEFISRYKSSGFIDLLHDKWYKMPCKGRVFAVTETLQMSY  
HFAGLFVLLCLGLSALLSSLGEHAFFRLALPRIRKGSRLQYWLHTSQKIERALNTEPPGSKHETAEAEF  
SGFEVEQQQQQDQPTAFEGWKARRAVDKERRVRFLEPAVVVAPEADAEAEAPREGPVWLCSYG  
RPPAARPTGAPQPGELQELERRIEVARERLRQALVRRGQLLAQLGDSARHRPRRLQARAAPAEAPPESG  
RPGSQE



FIG. 19

Score = 5188 (778.4 bits), Expect = 0.0, Sum P(4) = 0.0  
Identities = 1068/1092 (97%), Positives = 1068/1092 (97%), Strand = Plus / Plus

Query: 1019 GGTTCCTGGCCACACGTCCTTCACAGGCCGACAGGCCCCGTGTGGGTGACAGGCAGCT 1078  
GGTTCCTGGCCACACGTCCTTCACAGGCCGACAGGCCCCGTGTGGGTGACAGGCAGCT  
Sbjct: 22747 GGTTCCTGGCCACACGTCCTTCACAGGCCGACAGGCCCCGTGTGGGTGACAGGCAGCT 22806

Query: 1079 CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCCGGGACCCACGGGGCG 1138  
CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCCGGGACCCACGGGGCG  
Sbjct: 22807 CCCAGGTACACATGTCTCGGCACCTTTAAGGTGTGGAGCCTTCGCCGGGACCCACGGGGCG 22866

Query: 1139 CCCCCGCTGGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGCACCGGGAG 1198  
CCCCCGCTGGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGCACCGGGAG  
Sbjct: 22867 CCCCCGCTGGGCCACGGTGGGCAGCTGGCGGGACGGCCAGCTGGACTTGCACCGGGAG 22928

Query: 1199 GTGCTCTGCACGCCCCCCCCCCCCACAGGGTGCCTAGGTCTGGCCCAAGCTGCGTGTGG 1258  
GTGCTCTGCACGCCCCCCCCCCCCACAGGGTGCCTAGGTCTGGCCCAAGCTGCGTGTGG  
Sbjct: 22927 GTGCTCTGCACGCCCCCCCCCCCCACAGGGTGCCTAGGTCTGGCCCAAGCTGCGTGTGG 22986

Query: 1259 TAAGGCTGTTCGAACACCCATTGTGTGTTGCCCGTGTATCCAGACGAAGACGGCCAGTGGC 1318  
TAAGGCTGTTCGAACACCCATTGTGTGTTGCCCGTGTATCCAGACGAAGACGGCCAGTGGC  
Sbjct: 22987 TAAGGCTGTTCGAACACCCATTGTGTGTTGCCCGTGTATCCAGACGAAGACGGCCAGTGGC 23046

Query: 1319 CAGCGGGGCACTGTGCTTGCACCCCTGGCACCACGACTCGGCCACCCCTGGACGCACTGT 1378  
CAGCGGGGCACTGTGCTTGCACCCCTGGCACCACGACTCGGCCACCCCTGGACGCACTGT  
Sbjct: 23047 CAGCGGGGCACTGTGCTTGCACCCCTGGCACCACGACTCGGCCACCCCTGGACGCACTGT 23106

Query: 1379 TCGCCGGCTGGCCACGGCTCAGCGCCCCGTGCCCTGCCCAAGTCTGCTACGGCTACT 1438  
TCGCCGGCTGGCCACGGCTCAGCGCCCCGTGCCCTGCCCAAGTCTGCTACGGCTACT  
Sbjct: 23107 TCGCCGGCTGGCCACGGCTCAGCGCCCCGTGCCCTGCCCAAGTCTGCTACGGCTACT 23166





FIG. 19 Continued

Query: 1439 GCATTGACCTGCTGGAGCGGCTGGCGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG 1498  
GCATTGACCTGCTGGAGCGGCTGGCGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG  
Sbjct: 23167 GCATTGACCTGCTGGAGCGGCTGGCGAGGACACGCCCTTCGACTTCGAGCTGTACCTCG 23226

Query: 1499 TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCCTGACCGGCTTGGTCCGGGACC 1558  
TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCCTGACCGGCTTGGTCCGGGACC  
Sbjct: 23227 TGGGTGACGGCAAGTACGGCGCCCTGCGGGACGGCCCTGACCGGCTTGGTCCGGGACC 23286

Query: 1559 TGCTGCCCGGCGGCGGCCACATGGCGGTACCCAGCTTCAGTATCAACTCCGCCCGCTCAC 1618  
TGCTGCCCGGCGGCGGCCACATGGCGGTACCCAGCTTCAGTATCAACTCCGCCCGCTCAC  
Sbjct: 23287 TGCTGCCCGGCGGCGGCCACATGGCGGTACCCAGCTTCAGTATCAACTCCGCCCGCTCAC 23346

Query: 1619 AAGTGGTGGACTTCACCAGCCCCCTTCTTCTCCACCAGCCTGGGCATCATGGTCCGGGCAC 1678  
AAGTGGTGGACTTCACCAGCCCCCTTCTTCTCCACCAGCCTGGGCATCATGGTCCGGGCAC  
Sbjct: 23347 AAGTGGTGGACTTCACCAGCCCCCTTCTTCTCCACCAGCCTGGGCATCATGGTCCGGGCAC 23406

Query: 1679 GGGACACGGGCTCACCCATCGGTGCTTTATGTGGCCCTGCACCTGGTCCAGGTGGCTGG 1738  
GGGACACGGGCTCACCCATCGGTGCTTTATGTGGCCCTGCACCTGGTCCAGGTGGCTGG  
Sbjct: 23407 GGGACACGGGCTCACCCATCGGTGCTTTATGTGGCCCTGCACCTGGTCCAGGTGGCTGG 23466

Query: 1739 GCGTCTTTGCGGCGCTGCACCTCACCGGCTCTTCTCACCGTGTACAGTGGCGTAGCC 1798  
GCGTCTTTGCGGCGCTGCACCTCACCGGCTCTTCTCACCGTGTACAGTGGCGTAGCC  
Sbjct: 23467 GCGTCTTTGCGGCGCTGCACCTCACCGGCTCTTCTCACCGTGTACAGTGGCGTAGCC 23526

Query: 1799 CCTACGGGCTCACGCCACGTGGCGGCAACCGCAGCAGCTGTCTCTCTACTCTCTACGCC 1858  
CCTACGGGCTCACGCCACGTGGCGGCAACCGCAGCAGCTGTCTCTCTACTCTCTACGCC  
Sbjct: 23527 CCTACGGGCTCACGCCACGTGGCGGCAACCGCAGCAGCTGTCTCTCTACTCTCTACGCC 23586

Query: 1859 TCAACCTGTGCTACGCCATCCTCTTTCAGACGCACCGTGTCCAGCAAGACGCCCAAGTGCC 1918  
TCAACCTGTGCTACGCCATCCTCTTTCAGACGCACCGTGTCCAGCAAGACGCCCAAGTGCC  
Sbjct: 23587 TCAACCTGTGCTACGCCATCCTCTTTCAGACGCACCGTGTCCAGCAAGACGCCCAAGTGCC 23646

Query: 1919 CCACGGGCGGCTGCTCATGAACCTCTGGGCCATCTTCTGCTGCTGGTGTCTTCCAGCT 1978  
CCACGGGCGGCTGCTCATGAACCTCTGGGCCATCTTCTGCTGCTGGTGTCTTCCAGCT  
Sbjct: 23647 CCACGGGCGGCTGCTCATGAACCTCTGGGCCATCTTCTGCTGCTGGTGTCTTCCAGCT 23706

Query: 1979 ACACGGCCAACTGGCTGCCGTATGGTGGGGACAAGACCTTCGAGGAGCTGTGGGGA 2038  
ACACGGCCAACTGGCTGCCGTATGGTGGGGACAAGACCTTCGAGGAGCTGTGGGGA  
Sbjct: 23707 ACACGGCCAACTGGCTGCCGTATGGTGGGGACAAGACCTTCGAGGAGCTGTGGGGA 23766

Query: 2039 TCCACGACCCCAAGCTGCACACC-CGGCGCAGGGCTTCGGCTTCGGCACCCTGTGGGAG 2097  
TCCACGACCCCAAG T8 C CC CG G GGGCT C G T GGC G G GGG  
Sbjct: 23767 TCCACGACCCCAAGTGGCGGGCTTCGG-G--GGGCTGGGGT--GGGCTTGGG-GGGCT 23820

Query: 2098 AGCAGCG-CGGAG 2110  
AGC G G CC GG  
Sbjct: 23821 AGCGGTGGCCCCG 23834



FIG. 20

Score = 4730 (1665.0 bits), Expect = 0.0, P = 0.0  
Identities = 900/900 (100%), Positives = 900/900 (100%), Frame = +1

Query: 1 HEFVRALMIGLALALGPGSAGGHPQPCGVLARLOGSVRLGALLPRAFLARARARALARA 180  
HEFVRALMIGLALALGPGSAGGHPQPCGVLARLOGSVRLGALLPRAFLARARARALARA  
Sbjct: 1 HEFVRALMIGLALALGPGSAGGHPQPCGVLARLOGSVRLGALLPRAFLARARARALARA 60

Query: 181 ALAPRLPHNLSLELVVAAPPARDPASL/TRGLCOALVPPGVAALLAPPEARPELLQLHFLA 360  
ALAPRLPHNLSLELVVAAPPARDPASL/TRGLCOALVPPGVAALLAPPEARPELLQLHFLA  
Sbjct: 61 ALAPRLPHNLSLELVVAAPPARDPASL/TRGLCOALVPPGVAALLAPPEARPELLQLHFLA 120

Query: 361 AATETPVLSLLRREARAPLGAPNPFHLQLHNASPLETLLDVLVAVLQAHAMEDVGLALCR 540  
AATETPVLSLLRREARAPLGAPNPFHLQLHNASPLETLLDVLVAVLQAHAMEDVGLALCR  
Sbjct: 121 AATETPVLSLLRREARAPLGAPNPFHLQLHNASPLETLLDVLVAVLQAHAMEDVGLALCR 180

Query: 541 TQDPGGLVALNTRAGRPQQLVLDLSRDTGDAGLRARLAPMAAPVGGEAPVPAVLLGC 720  
TQDPGGLVALNTRAGRPQQLVLDLSRDTGDAGLRARLAPMAAPVGGEAPVPAVLLGC  
Sbjct: 181 TQDPGGLVALNTRAGRPQQLVLDLSRDTGDAGLRARLAPMAAPVGGEAPVPAVLLGC 240

Query: 721 DIARARKVLEAVFPQPHMLLQTFPLPKALPTACLPPCLLALGEVARPFLAATHDIVQLV 900  
DIARARKVLEAVFPQPHMLLQTFPLPKALPTACLPPCLLALGEVARPFLAATHDIVQLV  
Sbjct: 241 DIARARKVLEAVFPQPHMLLQTFPLPKALPTACLPPCLLALGEVARPFLAATHDIVQLV 300

Query: 901 ARALGSAAGVQPKRALLPAFVNCGLQAGPESPGRTFLARFLANTSFGQRTGPPVWTGSS 1080  
ARALGSAAGVQPKRALLPAFVNCGLQAGPESPGRTFLARFLANTSFGQRTGPPVWTGSS  
Sbjct: 301 ARALGSAAGVQPKRALLPAFVNCGLQAGPESPGRTFLARFLANTSFGQRTGPPVWTGSS 360

Query: 1081 QVHMSRHFKVWSLRDPRGAPAMATVGSWEDGQLDLEFGGASARPPFPQGAQVWPKLRV 1260  
QVHMSRHFKVWSLRDPRGAPAMATVGSWEDGQLDLEFGGASARPPFPQGAQVWPKLRV  
Sbjct: 361 QVHMSRHFKVWSLRDPRGAPAMATVGSWEDGQLDLEFGGASARPPFPQGAQVWPKLRV 420

Query: 1261 TLLSHFFVFARDPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCTGYC 1440  
TLLSHFFVFARDPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCTGYC  
Sbjct: 421 TLLSHFFVFARDPDEDGQCPAGQLCLDPGTNDSATLDALFAALANGSAPRALRKCCTGYC 480

Query: 1441 IDLLERLAEDTFFDFELYVGDGKYGALDGRWTGLVGDLLAGRAHMAVTSFSINSARSQ 1620  
IDLLERLAEDTFFDFELYVGDGKYGALDGRWTGLVGDLLAGRAHMAVTSFSINSARSQ  
Sbjct: 481 IDLLERLAEDTFFDFELYVGDGKYGALDGRWTGLVGDLLAGRAHMAVTSFSINSARSQ 540



FIG. 20 Continued

Query: 1621 VVDFTSPFFSTSLGDMVRARDTASPIGAFHNFLENSTWLGVTAAALHLTALFLTVYENRSP 1800  
VVDFTSPFFSTSLGDMVRARDTASPIGAFHNFLENSTWLGVTAAALHLTALFLTVYENRSP  
Sbjct: 541 VVDFTSPFFSTSLGDMVRARDTASPIGAFHNFLENSTWLGVTAAALHLTALFLTVYENRSP 600

Query: 1801 YGLTPRGNRSTVFTSYSSALMLCYAILFRRTVSSKTPKCPGRLNNHMAIFCLLVLSY 1980  
YGLTPRGNRSTVFTSYSSALMLCYAILFRRTVSSKTPKCPGRLNNHMAIFCLLVLSY  
Sbjct: 601 YGLTPRGNRSTVFTSYSSALMLCYAILFRRTVSSKTPKCPGRLNNHMAIFCLLVLSY 660

Query: 1981 TANLAAMVVGDKTFEELSGIHDPKLHHPAQGFAPGTVWESSAEAYIKKSPFDMHAMRRH 2160  
TANLAAMVVGDKTFEELSGIHDPKLHHPAQGFAPGTVWESSAEAYIKKSPFDMHAMRRH  
Sbjct: 661 TANLAAMVVGDKTFEELSGIHDPKLHHPAQGFAPGTVWESSAEAYIKKSPFDMHAMRRH 720

Query: 2161 SAPTTFRGVAMLTSDPPKLNAPINDKSLDYEVSIDADCKLLTVGKPPAIBGYGIGLPQN 2340  
SAPTTFRGVAMLTSDPPKLNAPINDKSLDYEVSIDADCKLLTVGKPPAIBGYGIGLPQN  
Sbjct: 721 SAPTTFRGVAMLTSDPPKLNAPINDKSLDYEVSIDADCKLLTVGKPPAIBGYGIGLPQN 780

Query: 2341 SPLTSHLSEFISRYKSSGPFIDLLHDKWYQIVPCGRVFAVTETLQMSIYHPAGLFVLLCL 2520  
SPLTSHLSEFISRYKSSGPFIDLLHDKWYQIVPCGRVFAVTETLQMSIYHPAGLFVLLCL  
Sbjct: 781 SPLTSHLSEFISRYKSSGPFIDLLHDKWYQIVPCGRVFAVTETLQMSIYHPAGLFVLLCL 840

Query: 2521 GLGSALLSSLGERAFFRLALPRIRKGSRLQYWLHTSQKIHRAINTEPPGSKKETARAP 2700  
GLGSALLSSLGERAFFRLALPRIRKGSRLQYWLHTSQKIHRAINTEPPGSKKETARAP  
Sbjct: 841 GLGSALLSSLGERAFFRLALPRIRKGSRLQYWLHTSQKIHRAINTEPPGSKKETARAP 900



FIG. 21

Glutamate Receptor\_RAT\_AAD4163  
Glutamate Receptor\_Human\_06039  
21639239\_JC13  
ERRSLWLSRCLLPICALVLAEPSSSSPQPCQLEKSHANVWPAHLPQWTT  
EFUFAEWLALAGS.....AASHPC7CGLARDGTSWELCALCP.....  
EFUFAEWLALAGS.....AASHPC7CGLARDGTSWELCALCP.....

Glutamate Receptor\_RAT\_AAD4163  
Glutamate Receptor\_Human\_06039  
21639239\_JC13  
RASRQEQGRMAQDDPSQYWRPPASQGARWLSPHSDPPSSKLGGAQAE  
RLARRA.....RAARAR.....  
RLARRA.....RAARAR.....

Glutamate Receptor\_RAT\_AAD4163  
Glutamate Receptor\_Human\_06039  
21639239\_JC13  
YIWPEDALIFAVENLHRVEGLTYLLELQWLEIKAOLQDLPLMDPSSPSSPWISLTP  
.....THHLEEDVAAH.....  
.....THHLEEDVAAH.....

Glutamate Receptor\_RAT\_AAD4163  
Glutamate Receptor\_Human\_06039  
21639239\_JC13  
LOSHTYVVOVSCDAEIQSQOEHLHLSVLIHITCDEEY..PRESQLE  
EFGLOALVVOUVAALLAFDEARFELLQHSAAWAEEDHISLSSPAAALUGQNDL  
EFGLOALVVOUVAALLAFDEARFELLQHSAAWAEEDHISLSSPAAALUGQNDL

Glutamate Receptor\_RAT\_AAD4163  
Glutamate Receptor\_Human\_06039  
21639239\_JC13  
SLENSSDAETSTMMNHYNFSLEQEDWHITDFLLCHNSKTHLESNN  
LHNWASPLTILLDLYAVIQAHAWEDVGLACRTQDGGOLVALWTRAG..LDRWQD  
LHNWASPLTILLDLYAVIQAHAWEDVGLACRTQDGGOLVALWTRAG..LDRWQD

Glutamate Receptor\_RAT\_AAD4163  
Glutamate Receptor\_Human\_06039  
21639239\_JC13  
ANLSTKDELSPQVQMDHER..NSTLHHTFEDNDSIQDEASTQFG..LPLW  
RROTCQAPDPAALIAHATFUGGCAFUFANQCCDPAHPEHDE.....V  
RROTCQAPDPAALIAHATFUGGCAFUFANQCCDPAHPEHDE.....V

Glutamate Receptor\_RAT\_AAD4163  
Glutamate Receptor\_Human\_06039  
21639239\_JC13  
DSQHVKELEELSLSEHKKTIQSVYTHQSALETCARFANSTLHST  
EELHHAATAGLITGLALGEVARTTEKANNHIVGLWALGTAARVCFATLUTN  
EELHHAATAGLITGLALGEVARTTEKANNHIVGLWALGTAARVCFATLUTN

Glutamate Receptor\_RAT\_AAD4163  
Glutamate Receptor\_Human\_06039  
21639239\_JC13  
NCHLTKTTHLLEQLHSEFLANHEDLSEHKLKILLSSKIPFESFTEFLK  
NHCCELPAGEESTFELARPLANTSPQSSQWWTGSSQTHHHPHAWLPSHIG  
NHCCELPAGEESTFELARPLANTSPQSSQWWTGSSQTHHHPHAWLPSHIG

Glutamate Receptor\_RAT\_AAD4163  
Glutamate Receptor\_Human\_06039  
21639239\_JC13  
LSTREPSWOCRLVHNSIWPQQAQHKYTHQHPMKLEHVVTLSDPFWTFLV  
LAWTVSGWGLSRDCCCEP...SASARHISGQAQWHEHVVTLSDPFWTFLV  
LAWTVSGWGLSRDCCCEP...SASARHISGQAQWHEHVVTLSDPFWTFLV

Glutamate Receptor\_RAT\_AAD4163  
Glutamate Receptor\_Human\_06039  
21639239\_JC13  
LTFACGLCLDLPDQSMTRHSSSSSSNDVLIKFBHGVVCHLLEQWAEALF  
NCFACGLCLDLPDQSMTRHSSSSSSNDVLIKFBHGVVCHLLEQWAEALF  
NCFACGLCLDLPDQSMTRHSSSSSSNDVLIKFBHGVVCHLLEQWAEALF

Glutamate Receptor\_RAT\_AAD4163  
Glutamate Receptor\_Human\_06039  
21639239\_JC13  
DEYVWDCHHGAELHSHHTGLVODLUSITLAVTSPSINARSQVCFPTSPHSDLG  
EVLVWDCHHGAELHSHHTGLVODLUSITLAVTSPSINARSQVCFPTSPHSDLG  
EVLVWDCHHGAELHSHHTGLVODLUSITLAVTSPSINARSQVCFPTSPHSDLG



FIG. 22

21659259\_EXT\_3 MEEVRAIWLGLALALGPGSAGGHPOCGVLAELGGSVRLGALLPRAPLAKARAKALARA  
21659259\_EXT\_2 MEEVRAIWLGLALALGPGSAGGHPOCGVLAELGGSVRLGALLPRAPLAKARAKALARA  
21659259\_EXT\_1 MEEVRAIWLGLALALGPGSAGGHPOCGVLAELGGSVRLGALLPRAPLAKARAKALARA  
21659259\_EXT\_3 ALAPRLPHNLSTELVVAAPPARDPASTTRGLGQALVPPGVAAALAEFEARPELLQLHFLA  
21659259\_EXT\_2 ALAPRLPHNLSTELVVAAPPARDPASTTRGLGQALVPPGVAAALAEFEARPELLQLHFLA  
21659259\_EXT\_1 ALAPRLPHNLSTELVVAAPPARDPASTTRGLGQALVPPGVAAALAEFEARPELLQLHFLA  
21659259\_EXT\_3 AATEPVLSTLRREARAPLGAPNPHLQLHWAASPLELLDVLVAVLQAHAWEDVGLALGR  
21659259\_EXT\_2 AATEPVLSTLRREARAPLGAPNPHLQLHWAASPLELLDVLVAVLQAHAWEDVGLALGR  
21659259\_EXT\_1 AATEPVLSTLRREARAPLGAPNPHLQLHWAASPLELLDVLVAVLQAHAWEDVGLALGR  
21659259\_EXT\_3 TODPGLVALWTSRAGRPPQLVLDLSKRDIGDAGLRLAPMAAVGGEAPVPAVAVLGG  
21659259\_EXT\_2 TODPGLVALWTSRAGRPPQLVLDLSKRDIGDAGLRLAPMAAVGGEAPVPAVAVLGG  
21659259\_EXT\_1 TODPGLVALWTSRAGRPPQLVLDLSKRDIGDAGLRLAPMAAVGGEAPVPAVAVLGG  
21659259\_EXT\_3 DIARARVLEAVPPGPHWLLGTPPKALPTAGLPPGLLALGEVARPLEAATHDIVQLV  
21659259\_EXT\_2 DIARARVLEAVPPGPHWLLGTPPKALPTAGLPPGLLALGEVARPLEAATHDIVQLV  
21659259\_EXT\_1 DIARARVLEAVPPGPHWLLGTPPKALPTAGLPPGLLALGEVARPLEAATHDIVQLV  
21659259\_EXT\_3 ARALGSAAQVOPKRALPAFVNGGDLQOPAGPESPGRELARELANTSFOGRTPVWVTGSS  
21659259\_EXT\_2 ARALGSAAQVOPKRALPAFVNGGDLQOPAGPESPGRELARELANTSFOGRTPVWVTGSS  
21659259\_EXT\_1 ARALGSAAQVOPKRALPAFVNGGDLQOPAGPESPGRELARELANTSFOGRTPVWVTGSS  
21659259\_EXT\_3 QVHMSRHFVWSLRKDPKCAPAWATVGSWRDGLDLBFGGASALPPPPQGAQVWPELNAV  
21659259\_EXT\_2 QVHMSRHFVWSLRKDPKCAPAWATVGSWRDGLDLBFGGASALPPPPQGAQVWPELNAV  
21659259\_EXT\_1 QVHMSRHFVWSLRKDPKCAPAWATVGSWRDGLDLBFGGASALPPPPQGAQVWPELNAV  
21659259\_EXT\_3 TLLBHPVFARDPDEDGQCPAGQGLGDPGINDSAILDALFAALANGSAPRALRGYGYC  
21659259\_EXT\_2 TLLBHPVFARDPDEDGQCPAGQGLGDPGINDSAILDALFAALANGSAPRALRGYGYC  
21659259\_EXT\_1 TLLBHPVFARDPDEDGQCPAGQGLGDPGINDSAILDALFAALANGSAPRALRGYGYC



## FIG. 22 Continued

21659259_EXT_3	RLLQARAAPAEAPPHSGRPGSQE
21659259_EXT_2	RLLQARAAPAEAPPHSGRPGSQE
21659259_EXT_1	RLLQARAAPAEAPPHSGRPGSQE



FIG. 23

ACGCGTTACTCCTACCAGGTTGTAGCATGCATCTTTTTGAGAGAGCAGCTGGGATCGAGTA  
TACTCTTGACTTAAATATGTTTGTATAAAGACAAATGGAGAAATCAATTTTTCCCTGA  
ATTCTTAGGAGCACTTTAGTGAATAAAGAACCTGACAGTATGCTGGGCCACATGTTAAGG  
ACAAAGGTGTCTGGGGAATAAGCAAGATCATAGAGGAGCTTTCTTAATTGACCGAAGTCC  
TGAGTACTTCGAACCCATTTGAACTACTTGCCTCATGGACAGCTCATTGTAAATGATGGCA  
TTAATTTATTGGGTGTGTTAGAAGAAGCAAGATTTTTGGTATTGACTCATTGATGAACAC  
CTAGAAGTGGCAATAAAGAATTCTCAACCACCGGAGGATCATTACCAATATCCCGAAAGG  
AAATTTGTCCGATTTTTGCTAGCAACTCCAACCAAGTCAGAACTGCGATGCCAGGGTTTGAA  
CTTCAGTGGTGTGATCTTTCTCGTTTGGACCTTCGATACATTAACCTCAAAATGGCCAATT  
TAAGCCGCTGTAATCTTGCACATGCAAATCTTTGCTGTGCAAATCTTGAACGAGCTGATCTC  
TCTGGATCAGTGCTTGACTGTGCGAATCTCCAGGGAGTCAAGATGCTCTGTTCTAATGCAG  
AAGGAGCATCCCTGAAACTGTGTAATTTGAGGATCCTTCTGGTCTTAAAGCCAATTTAGA  
AGGTGCTAATCTGAAAAGGTGTGGATATGGAAGGAAGTCAGATGACAGGAATTAACCTGAG  
AGTGGCTACCTTAAAAAATGCAAAGTTGAAGAAGTGTAACTCAGAGGAGCAACTCTGGC  
AGGAACTGATTTAGAGAATTGTGATCTGTCTGGGTGTGATCTTCAAGAAGCCAACCTGAGA  
GGGTCCAACGTGAAGGGAGCTATATTGAAGAGATGCTGACACCACTACACATGTACAAAA  
GTGTCAGATGAGAATTTTAGGGGCTGGAGGAAGATGTAAAAGATGAAAATGTTTTCTTAT  
CACTTTTCTTTCTCCACCCACTCAGTTGTCTAGAAGAAATAACACTGTAAGGAAATTTAAAA  
AAAAAAA



FIG. 24

MLAHMPKDKGVWGNKQDHRGAFLIDRSPEYFEPILNYLRHGQLIVNDGINLLGVLEEARFFGID  
SLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELRCQGLNFGADLSRLDLRYNFKMAN  
LSRCNLAHANLCCANLERADLSGSVLDGANLQGVKMLCSNABGASLKLCNFEDPSGLKANLE  
GANLKGVDMEGSQMTGINLRVATLKNAKLKNCNLRGATLAGTDLENCDSLGCIDLQEANLRGS  
NVKGAIFEEMLTPLHMSQSVR



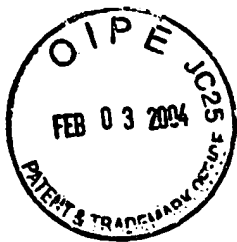


FIG. 25

Score = 1486 (523.1 bits), Expect =  $1.4e-151$ , P =  $1.4e-151$   
Identities = 286/286 (100%), Positives = 286/286 (100%), Frame  
= +1

Query: 130 RSTLVNKEPDSMLAHMPKDGWGNKQDHGAPLIDRSPFYTFPIILTYLRHQQLIVHDGI 309  
RSTLVNKEPDSMLAHMPKDGWGNKQDHGAPLIDRSPFYTFPIILTYLRHQQLIVHDGI  
Sbjct: 104 RSTLVNKEPDSMLAHMPKDGWGNKQDHGAPLIDRSPFYTFPIILTYLRHQQLIVHDGI 163

Query: 310 NLLGVLEEARPPGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELRCQGL 489  
NLLGVLEEARPPGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELRCQGL  
Sbjct: 164 NLLGVLEEARPPGIDSLIEHLEVAIKNSQPPEDHSPISRKEFVRFLATPTKSELRCQGL 223

Query: 490 NPSGADLSRLDLRYINFIOMANLSRCHLAHANLCCANLERADLSGSVLDGANLQGVVHLC 669  
NPSGADLSRLDLRYINFIOMANLSRCHLAHANLCCANLERADLSGSVLDGANLQGVVHLC  
Sbjct: 224 NPSGADLSRLDLRYINFIOMANLSRCHLAHANLCCANLERADLSGSVLDGANLQGVVHLC 283

Query: 670 NAEASLKLCHNFDPSGLKANLEGANLKGVDMEGSMGTGINLEVATLKQAKLQCHLGA 849  
NAEASLKLCHNFDPSGLKANLEGANLKGVDMEGSMGTGINLEVATLKQAKLQCHLGA  
Sbjct: 284 NAEASLKLCHNFDPSGLKANLEGANLKGVDMEGSMGTGINLEVATLKQAKLQCHLGA 343

Query: 850 TLAGTDLENCDLSQCDLQEAHLRGSFVGAIFEEMLITPLHMSQSVR 987  
TLAGTDLENCDLSQCDLQEAHLRGSFVGAIFEEMLITPLHMSQSVR  
Sbjct: 344 TLAGTDLENCDLSQCDLQEAHLRGSFVGAIFEEMLITPLHMSQSVR 389

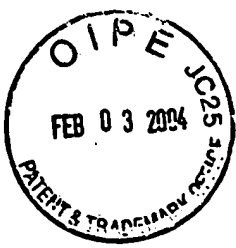
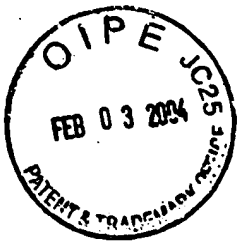


FIG. 26

TTCCAGGGTTCTAGCCTGTTTCATCTAGCCCCATGATGGCTGTGGACATCGAGTACAGATACAACCTGCAT  
GGCTCCTTCCTTGCGCCAAGAGAGGTTTGCCTTTAAGATCTCACAAAGCCCAGCAAACCACTGAGGCCT  
TGTATTCACTGAGCAGCAAGAATGAAGCCAGTGAATGGTGGCCCCGGCTGTCCAGGAGAAGAAGGTGA  
AAAAGCGGGTGTCTTCGCAGACAACCAGGGGCTGGCCCTGACAATGGTCAAAGTGTTCGGAATTCTGA  
TGACCCGCTAGATATGCCATTCAACATCACCGAGCTCCTAGACAACATTGTGAGCTTGACGACAGCAGAG  
AGCGAGAGCTTTGTTCTGGATTTTTCCAGCCCTCTGCAGATTACTTAGACTTTAGAAATCGACTTCAGG  
CCGACCACGCTGCCTTGAGAACTGTGTGCTCAAGGACAAGGCCATTGCAGGCACTGTGAAGGTTTCAGAA  
CCTCGCATTTGAGAAGACCGTGAAAATAAGGATGACGTTTCGACACCTGGAAGAGCTACACAGACTTTTCCT  
TGTCACTACGTGAAGGACACTTATGCCGGTTTCAGACAGGGACACGTTCTCCTTCGACATCAGCTTGCCCCG  
AGAAGATTCAGTCTTATGAAAGAATGGAGTTTGCTGTGTACTACGAGTGCAATGGACAGACGTAAGGGA  
CAGCAACAGAGGCAAGAATATAGGATCATCCGGCTGAGTTAAATCTACCCAGGGAATGACCAAGCCC  
CACAGTGGACCGGATTTGGGAATATCCTTTGACCAGTTCCGAAGCCCTCGGTGTTCTATGGTCTGTTTC  
CAGAGTGGCCAAGTTACTTAGGATATGAAAAGCTAGGGCCCTACTACTAATGACTGCAGGTGACAGGGCG  
TGGCGGAGCTGCCACA



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**FIG. 27**

MMAVDIEYRYNCMAPSLRQERFAFKISPKPSKPLRPCIQLSSKNEASGMVAPAVQEKVKRVSFADNQG  
LALTMVKVFSEFDDPLDMPFNITELLDNIVSLTTAESSEFVLDFSQPSADYLDNRNLQADHVCLENCVL  
KDKALAGTVKVQNLAFKTVKIRMTFDTWKS YTDFFCQYVKDTYAGSDRDTFSFDISLPEKIQSYERMEF  
AVYYECNGQTYWDSNRGKNYRIIRAEKSTQGMTKPHSGPDLGISFDQFGSPRC SYGLFPEWPSYLGYEK  
LGPYY

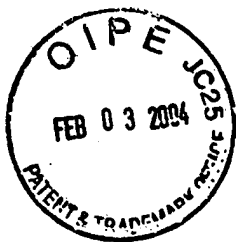


FIG. 28

Score = 3195 (479.4 bits), Expect = 2.8e-138, P = 2.8e-138  
Identities = 763/903 (84%), Positives = 763/903 (84%), Strand = Plus / Plus

Query: 6 AGGGTTCTAGCCTGTTTCATCTAGCCCCATGATGGCTGTGGACATCGAGTACAGATACAAC 65  
AG TTCTAGCCTG C TCTA C TGATGCG GTGGACAT GA TACAG TACA C  
Sbjct: 65 AGACTTCTAGCCTGCCCCCTCTAACG---TGATGGCCGTGGACATAGAATACAGCTACAGC 121

Query: 66 TGCATGGCTCCTTCTCTTGGGCCAAGAGAGTTTGGCTTTAAGATCTCACCAAGCCGAGC 125  
G ATGCG CCTC TGGC AGAG G TT CCTT AAGATCTC CC AA C A C  
Sbjct: 122 AGTATGGCCCCCTTCTCTGCGCAGAGAAGCGCTTCACCTTCAAGATCTCCCCCAACTGAAC 181

Query: 126 AAACCACTGAGGCTTGTATTTCAGCTGAGCAGCAAGAATGAAGCCAGTGGAAATGGTGGCC 185  
AA CCACTGAGGCTTGTATTTCAGCTG GACGCAAG ATGAAGCC G GAATGGTGGCC  
Sbjct: 182 AAGCCACTGAGGCTTGTATTTCAGCTGGGCAGCAAGGATGAAGCCGAGAAATGGTGGCC 241

Query: 186 CCGGCTGTCCAGGAGAAGAAGGTGAAAAAGCGGGTGTCTTCCAGACAAACAGGGGCTG 245  
CC C GT CAGGAGAGAAGGTGAA AAGCGGGTGTCTTCCG GACAAACAGGGGCTG  
Sbjct: 242 CCCACAGTACAGGAGAAGAAGGTGAAGAAGCGGGTGTCTTCCGACAAACAGGGGCTG 301

Query: 246 GCCCTGACAAATGGTCAAGTGTCTCGGAATTCGATGACCCCTAGATATGCCATTCAAC 305  
GCCCT ACAATGGT AAGTGTCTCGGAATTCGATGACCC CTAGATAT CC TT AAC  
Sbjct: 302 GCCCTAACAATGGTGAAGTGTCTCGGAATTCGATGACCCCTAGATATTCGGTTTAAAC 361

Query: 306 ATCACCGAGCTCCTAGACAACATTGTGAGCTTGACGACAGCAGAGAGCGAGAGCTTTGTT 365  
ATCAC GAGCTCCTAGACAACAT GTGAG TGACGACAGCAGAGAG GAGAGCTTTGTT  
Sbjct: 362 ATCACTGAGCTCCTAGACAACATCGTGAGCTTGACGACAGCAGAGAGTGAGAGCTTTGTT 421

Query: 366 CTGGATTTTCCCGAGCCCTCTGCAGATTACTTAGACTTTAGAAATCGACTTCAGGCCGAG 425  
TGGATTTT C CAGCC TCTGCAGATTACTTAGACTTTAGAAATCG CTTCAG CC AC  
Sbjct: 422 TCGATTTTCCCGAGCCCTCTGCAGATTACTTAGACTTTAGAAATCGGCTTCAGACCAAC 481

Query: 426 CACGTCTGCTTGAAGAACTGTGTCTCAAGGACAAGGCCATTGCAAGCACTGTGAAGGTT 485  
CA GTCTGCTT GA AACTG GTGCT AAGGA AA GCGAT CC GGCAC GT AAGGT  
Sbjct: 482 CATGTCTGCTTGAAGAACTGCGTGTCTGAAGGAGAAGGCCATCGCGGCACCGTCAAGGTC 541

Query: 486 CAGAACCTGCGATTTGAGAAGACCGTGAAAAATAAGGATGACGTTCCGACCTGGAAGAC 545  
CAGAACCT GCGATT GAGAAG GTGAA AT AG ATGAC TTGGA ACCTGGAAG AOC  
Sbjct: 542 CAGAACCTGCGATTTGAGAAGGTTGTGAAGATCAGCATGACATTGATACCTGGAAGAC 601

Query: 546 TACACAGACTTTCTTGTGAGTACGTTGAAGGACACTTATGCCGTTTCAGACAGGACAGC 605  
T CACAGACTT CCTTGTGAGTA GTGAAGGACACTTA GC GGTTCAGACAGGACAC  
Sbjct: 602 TTCACAGACTTTCTTGTGAGTATGTGAAGGACACTTACGCTGTTTCAGACAGGACACA 661

Query: 606 TTCTCCTTGGACATCAGCTTCCCGAGAAGATTCACTCTTATGAAGAATGGAGTTTCTCT 665  
TTCTCCTT GA ATCAGC T CC GAGAA AT CAGTCTTATGAAGAATGGAGTT CC  
Sbjct: 662 TTCTCCTTGTATATCAGCTTACCGGAGAAAATCCAGTCTTATGAAGAATGGAGTTCCGC 721

Query: 666 GTGTACTACGAGTGAATGGACAGAGCTACTGGGACAGCAACAGAGGCAAGAACTATAGG 725  
GTGT CTACGAGTG AA GG CAG CGTACTGGGACAGCAACA AGGCAA AACTA AGG  
Sbjct: 722 GTGTGCTACGAGTGAATGGCCAGTGTACTGGGACAGCAACAAAGGCAAAACTACAGG 781

Query: 726 ATCATCCGGGCTGAGTTAAATCTACCCAGGGGATGACCAAGCCCCACAGTGGACCGGAT 785  
ATCA C GGGC GA T A ATC ACCCAGGGAATGAC AGCC ACA TGG CCGAT  
Sbjct: 782 ATCACCAGGGCCGAATCAGATCCACCCAGGGAATGACTGAGCCGTACAATGGCCCGAT 841

Query: 786 TTGGGAATATCCTTTGACCAGTTGGAAGCCCTGGGTGTCTCTATGGTCTGTTTCCAGAG 845  
TT GGAAT TC TTGACCAGTTGG AGCCCTGGGTGTCTCT GG CTGTTTCCAGAG  
Sbjct: 842 TTGGGAATCTCTTTGACCAGTTGCGGAGCCCTGGGTGTCTCTGCGCTGTTTCCAGAG 901

Query: 846 TGGCCAAGTTACTTAGGATATGAAAAGCTAGGGCCCTACTACTAGTGA-----CTGCAGG 900  
TGGCC AGTAA T GG TATGAAAAGCT GGGCCCTA TACTAGTGA CTGCAG  
Sbjct: 902 TGGCCTAGTTATCTGGGTATGAAAAGCTGGGGCCCTATTACTAGTGAGTTGACTGCAAT 961

Query: 901 TGACAG 906  
TGACAG  
Sbjct: 962 TGACAG 967

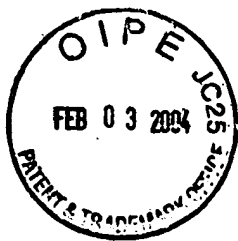


FIG. 29

Score = 1366 (480.9 bits), Expect = 1.3e-139, P = 1.3e-139  
Identities = 255/284 (89%), Positives = 270/284 (95%)

Query: 2 MAVDIEYRYNCHAPSLRQERPAFKISPKPSKPLRPCIQLSSKNEASGMVAPAVQEKVK 61  
MAVDIEY Y+ MAPSLR+ERF FKISPK +KPLRPCIQL SK+EA MVAP VQEKVK  
Sbjct: 1 MAVDIEYSYSSMAPSLRERPTFKISPKLNKPLRPCIQLGSKDEAGRMVAPTQEKVK 60

Query: 62 RVSFADNQGLALTMVKVFSEFDDPLDMPFNITELLDNIVSLTTAESESFVLDFSQPSADY 121  
RVSFADNQGLALTMVKVFSEFDDPLD+PFNITELLDNIVSLTTAESESFVLDF QPSADY  
Sbjct: 61 RVSFADNQGLALTMVKVFSEFDDPLDIPFNITELLDNIVSLTTAESESFVLDFPQPSADY 120

Query: 122 LDPRNRLQADHVCLENCVLKDKAIAAGTVKVNLAPEKTVKIRMTFDTWKS+TDFPCQYVK 181  
LDPRNRLQ +HVCLENCVLK+KAIAGTVKVNLAPEK VKIRMTFDTWKS+TDFPCQYVK  
Sbjct: 121 LDPRNRLQTNHVCLENCVLKEKAIAGTVKVNLAPEKVVKIRMTFDTWKSPTDFPCQYVK 180

Query: 182 DTYAGSDRDTFSFDISLPEKIQSYERMEFAVYECNQQTWDSNRGENYRIIRAELKSTQ 241  
DTYAGSDRDTFSFDISLPEKIQSYERMEFAV YECNQ+YWDSN+GENYRI RAEL+STQ  
Sbjct: 181 DTYAGSDRDTFSFDISLPEKIQSYERMEFAVCTECNQSYWDSNKGNYRITRAELKSTQ 240

Query: 242 GMTKPHSGPDLGISFDQFGSPRCSYGLFPEWPSYLGYEKLGPHY 285  
GMT+P++GPD GISFDQFGSPRCS+GLFPEWPSYLGYEKLGPHY  
Sbjct: 241 GMTPEYNGPDLGISFDQFGSPRCSFGLFPEWPSYLGYEKLGPHY 284



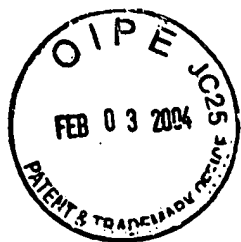


FIG. 31

CTGTCCTCGCATTCCTGAAACCTTCATCCACACAATGCCTCCCAACCTCACTGGC  
TACTACCGCTTTGTCTCGCAGAAGAACATGGAGGACTACCTGCAAGCCCTAAACATC  
AGCTTGGCTGTGCGGAAGATCGCGCTGCTGCTGAAGCCGGACAAGGAGATCGAACA  
CCAGGGCAACCACATGACGGTGAGGACGCTCAGCACCTTCGAAACTACACTGTGC  
AGTTGATGTGGGAGTGAGTTTGAGGAGGACCTCAGGAGCGTGGACGGACGAAAA  
TGCCAGATCTATTTCGTCGGTTCGGATCCAAGCCAGTTCTGTGGTCAGCAAGGCTCC  
CCTCTGGGCAGGCCCCCTGGTCAGAGGGAGTTTGTATCCTCAGGGAGGAGTTTGCGG  
CTGACCTTCGCGCACACAGCCTTCCTCGGAGAACAAAGACTGCCCCACCTCCACAAGGGC  
TTCTTGGCCCTCTACCAAACCGTGGCCTTAAGTGGAAGCTTGAGTGACAGCTGAGGC  
TGGGACTCAGGGACACCTGGGCTGGATCCCAGCCCTGCC

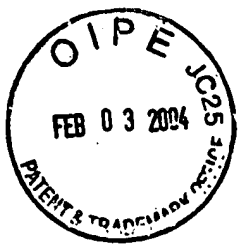


FIG. 32

MPPNLTGYRFFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFR  
NYTVQFDVGVEFEEDLRSVDGRKCQISFVGSDPSQFCGQQGSPLGRPPGQREFVSSGRSL  
RLTFRTQPSSSENKTAHLHKGFLALYQTVALSGSLSDS



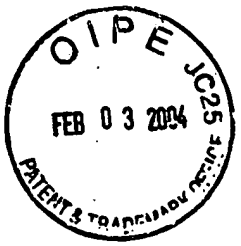


FIG. 33

Score = 355 (125.0 bits), Expect =  $1.0e-31$ , P =  $1.0e-31$   
Identities = 68/70 (97%), Positives = 70/70 (100%), Frame = +2

Query: 38 MPPFLTGYTRFVSQJOMEDYLQALNISLAVKIALLLKPKKEIEHQGHNTVRLSTYRN 217  
MPPFLTGYTRFVSQJOMEDYLQALNISLAVKIALLLKPKKEIEHQGHNTVRLSTYRN  
Sbjct: 1 MPPFLTGYTRFVSQJOMEDYLQALNISLAVKIALLLKPKKEIEHQGHNTVRLSTYRN 60

Query: 218 YTVQFDVGVE 247  
YV+QFDVGVE  
Sbjct: 61 YTVQFDVGVE 70



FIG. 34

CTGTCCTCTGCATTCTCCTGAAACCTTCATCCACACAATGCCTCCCAACCTCACTGGCTACTACCGCTTT  
GTCTCGCAGAAGAACATGGAGGACTACCTGCAAGCCCTAAACATCAGCTTGGCTGTGCGGAAGATCGCGC  
TGCTGCTGAAGCCGGACAAGGAGATCGAACACCAGGGCAACCACATGACGGTGAGGACGCTCAGCACCTT  
CCGAAACTACACTGTGCAGTTTGATGTGGGAGTGGAGTTTGAGGAGGACCTCAGGAGCGTGGACGGACGA  
AAATGCCAGACCATAGTAACCTGGGAGGAGGAGCACCTGGTGTGTGTGCAGAAAGGGGAGGTCCCCAACC  
GGGGCTGGAGACACTGGCTGGAGGGAGAGTTGCTGTATCTGGAACCTGACTGCAAGGGATGCAGTGTGCGA  
GCAGGTCTTCAGGAAGGTCAGATAGCCGGAGAGGAGCCAAGATCCCTCCAGACAGCACCAGCTCACAGAC  
GCTCTTGTGTGCCCCCTTCAAGCCCAGATTGTGCCAGATCTCATTCGTTCGGTTCGGATCCAAGCCAGTT  
CTGTGGTCAGCAAGGCTCCCCCTCTGGGCAGGCCCCCTGGTCAGAGGGAGTTTGTATCCTCAGGGAGGAGT  
TTGCGGCTGACCTTCCGCACACAGCCTTCCTCGGAGAAACAAGACTGCCACCTCCACAAGGGCTTCCTGG  
CCCTCTACCAAACCGTGGGTGAGTGTCCCTCCTGGGGGTGCAGGGAGGGAGCCTCTGTTCACAGCCATGA  
CCCTGGTATCTTCAAGCCTTAAGTGAAGCTTGAGTGACAGCTGAGG



FIG. 35

MPPNLTGYRFFVSQKNMEDYLQALNISLAVRKIALLLKPKETEHQGNHMTVRTLSTFRNYTVQFDVGVE  
FEEDLRSDGRKCQTIVTWEEHLVCVQKGEVFNRGWRHWLEGELLYLELTARDAVCEQVFRKVR



FIG. 36

Score = 712 (250.6 bits), Expect = 1.5e-69, P = 1.5e-69  
Identities = 133/135 (98%), Positives = 135/135 (100%), Frame =  
+2

Query: 38 MPPHLTGTYRFVSQKMEYTLQALNLSLAVRKIALLLKPKBIEHQGHMTVRTLSTFRN 217  
MPPHLTGTYRFVSQKMEYTLQALNLSLAVRKIALLLKPKBIEHQGHMTVRTLSTFRN  
Sbjct: 1 MPPHLTGTYRFVSQKMEYTLQALNLSLAVRKIALLLKPKBIEHQGHMTVRTLSTFRN 60

Query: 218 YTVQFDVGVVEFEEDLSVDGRKQQTIVTWEEHLVCVQKGEVPHRGWRHMLEGELLYLEL 397  
YT+QFDVGVVEFEEDLSVDGRKQQTIVTWEEHLVCVQKGEVPHRGWRHMLEG+LYLEL  
Sbjct: 61 YTLQFDVGVVEFEEDLSVDGRKQQTIVTWEEHLVCVQKGEVPHRGWRHMLEG+LYLEL 120

Query: 398 TARDVCEQVFRKVR 442  
TARDVCEQVFRKVR  
Sbjct: 121 TARDVCEQVFRKVR 135



FIG. 37

C018653\_A [REDACTED]  
C018653\_del\_ [REDACTED]  
C018653\_A [REDACTED] ISFVGS [REDACTED] PSQF [REDACTED] G [REDACTED] Q [REDACTED] S [REDACTED] P [REDACTED] L [REDACTED] G [REDACTED] E [REDACTED] Q [REDACTED] E [REDACTED] S [REDACTED] S [REDACTED] R  
C018653\_del\_ [REDACTED] TIVTWE [REDACTED] EHLV [REDACTED] V [REDACTED] K [REDACTED] EVPM [REDACTED] - [REDACTED] W [REDACTED] H [REDACTED] - [REDACTED] E [REDACTED] L [REDACTED] Y  
C018653\_A [REDACTED] TFRTQPSSSENKTAHLH [REDACTED] [REDACTED]  
C018653\_del\_ [REDACTED] ELTARDAVCEQVFRKV [REDACTED] .....